

WRI	MSEPP-----APPTPPPRH-----SSATFTIG-----DRISYFACDQ			
WRE	WQGRKALKLWFAA. FSTARTFLM. . VQ. PHIERLATI!!!. SCKLE. SP.CONTRY. E.			
WER1	AFPEE9--TPIQLE.A. POGZAVGCTSAATTHEALOLEELLE. EOCORRLEAFLTGQEV. LEB.			
WER2	WLAERFVLPALTIN. TIAEGPSFSEGASCELYVOLQKLELL. EOCORRLEAFLTGQEV. LEB.			
WER3	CCTPFSHHSNS-WSGSSCGGGFLAMTSKTVOKSGSLNFGAGYLJ. SRE. DFE.CLSSRATL. E			
Consensus				
	72	II	128	IV 142
WRI3	LVTISELCAGATGVVEVRAHQSGCTIAVERIAATVWSEQHQLLHLDLHTMTVCGTTVFTCALFREG			
WRI4	KDLG.L....S.H.VV.KP. Q.....S.OCR...C....VV..SS...F.I.G.			
WER1	TEK....A.EE...F.VS.EP. LV...E.L.MLEIRPAIRNG:122.CV-LMECSP. I.G....F130.			
WER2	FER....A.EG...T.VQ.EP..L...E.L.MLEIRPAIRNG:122.CV-LMECSP. I.G....F130.			
WER3	CFD...E.B...E.S.VL.KPTWV...T.EV. LELECAATQI...I.EV-LMECSP. I.G....F.I...			
Consensus	C 6 6 G V K N M A K		6	T V F T G A G
	143	V	171	
WRI3	DVWICHELG-TSLDKITF---EVLSQDNTIPEDILGEIAVSTTALENKQESLSVIRGQWEPILV.LHE			
WRI4	.C....S...F....STVTS...S-V...E...E.PLAT.E...S...KHN.EI....I....LSE			
WER1	EIS....E..GS...Q.....E.AGR...Q...EVSIASAVING.TV.NE.REIN.....I..V.S			
WER2	EIS....E..GS...Q.....E.AGR...E...EVSIASAVING.TV.NE.REIN.....I..V.S			
WER3	A.TH...T..GS....ITDSESSIEG----D.PQ.AF..HATING.EK.EQGQH....T.I.CSAE			
Consensus	CDE H S D	I E L	C L	HSD EP E L
	214	VEE	*	264
WRI3	CCWICHGIGSCTLVOSVARTHDQGCPHTAPERIHP-EUICRGTVVSVSLSITIUDIAI.LAVY--			
WRI4	S.H.L....Q...I...E...E...E...E...S.-SASQ...S.E.....LT.LTG....			
WER1	E.EI.L....V...Q.I...H.NSF-V.TRS...S...LOSTH----S.Q...I...H.LSLV...VG.T.IPF			
WER2	E.EI.L....V...Q.I...H.NSF-V.TRS....LOSTH----S.Q...I...H.LSLV...VG.T.IPF			
WER3	G.T.L....V...E...A.L....H.I...QH...ESLNFORAT.T...SLSI...LG.T....PF			
Consensus	G E CNG SG L I A S TN PER	T V S D W S G E A R P		
	285		X	359
WRI3	ESIG-----		-TPPOQJQWVCEPSPOLJAD--E	
WRI4	PK.E-----		-SV.B.T....NSGP....SSEERE	
WER1	PAKELEIAFQCGV---CEDAAETPPTRPTPGRPLSSTCHQSRPFFMAI.EI.SYI.H...P.R...SGV---			
WER2	PAKELEIAFQPVGGCGGEPMI3PMPFGRPVSGCHQSRPFFMAI.EI.SYI.H...P.R...SGV---			
WER3	TTB-----		-SI.S...SAI.SG.P.R.S...--E	
Consensus			F L V P L	
	336	II		426
WRI3	PSPEVYNTAACLAQKIPACQTLLEHCPPTTLESTKTDIAA.VK-----KILCQD			
WRI4	...S..IS..VKE...T..DESE..PK..E..LR...I..LNTEDRAVEV..C7..C.....SONPATPSSANTV			
WER1	...L..Q..VKE...I.....ADLGQ..V.A.IERSGAEV..P.GFCSTGQJQGQSTTVAAGV			
WER2	...L..Q..VKE...I.....ADLGQ..V.A.IERSGAEV..P.GFCSTGQJQGQSTTVAAGV			
WER3	...ADLGQ..VSL...Q.I.EK..PK..AA..T...PVLVETRQGQVQKSTTITLAEK...A..KEDCILSIVV7			
Consensus	C E G E L	I		

FIG. 1

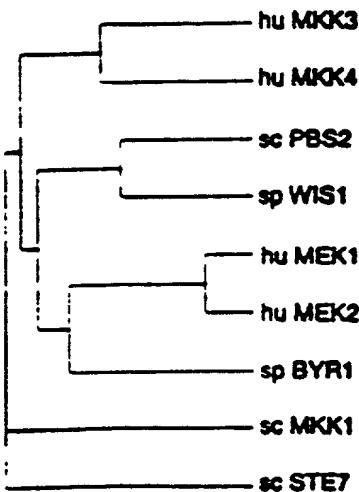


FIG. 2

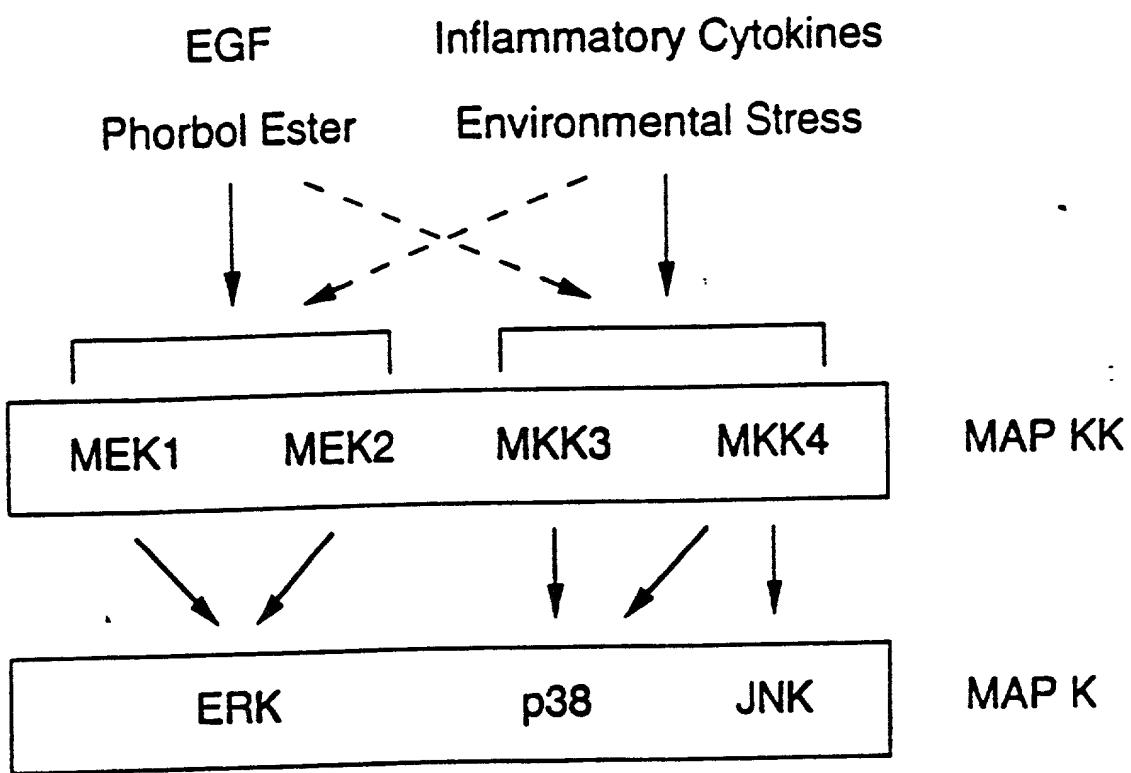


FIG. 3

FIG. 4

5	10	15	20	25	30	35	40	45	50	55	60
*	*	*	*	*	*	*	*	*	*	*	*
TGGCTGCCAA TGGCCTTGCT GACCTCGAGC CGGGCCCCACG TGGGGACCTT TGGAGCACAG											
ACCGACCCTT ACCCGAACGA CTGGAGCTCG GCCCGGGTGC ACCCCTGGAA ACCTCGTGTC											
65	70	75	80	85	90	95	100	105	110	115	120
*	*	*	*	*	*	*	*	*	*	*	*
CCTACGATCC TGGTGCAAGG CCGGTGGATG CAGAGGCCAG TCCATATAACC ACCCAGGGCT											
GGATGCTAGG ACCACGTTCC GGCCACCTAC GTCTCCGGTC AGGTATAATGG TGGGTCCGGA											
125	130	135	140	145	150	155	160	165	170	175	180
*	*	*	*	*	*	*	*	*	*	*	*
GCGAGGAGCG TGGTCCCCAC CCATCCAGCC CATATGTGCA AGTGCCTTG ACAGAGAGGC											
GGCTCCTCGC ACCAGGGGTG GGTAGGTGCG GTATACACGT TCACGGGAAC TGTCTCTCCG											
185	190	195	200	205	210	215	220	225	230	235	240
*	*	*	*	*	*	*	*	*	*	*	*
TGGTCATATC CATGGTGACC ATTTATGGGC CACAACAGGT CCCCATCTGC GCAGTGAACC											
ACCAGTATAG GTACCACTGG TAAATACCCG GTGTTGTCCA GGGTAGACG CGTCACTTGG											
245	250	255	260	265	270	275	280	285	290	295	300
*	*	*	*	*	*	*	*	*	*	*	*
CTGTGCTGAG CACCTTGAG ACGTGATCTT GCTTCGTCCT GCAGCACTGT GCGGGGCAGG											
GACACGACTC GTGGAACGTC TGCAGTAGAA CGAAGCAGGA CGTCGTGACA CGCCCCGTCC											
305	310	315	320	325	330	335	340	345	350	355	
*	*	*	*	*	*	*	*	*	*	*	
AAAATCCAAG AGGAAGAAGG ATCTACGGAT ATCCTGC ATG TCC AAG CCA CCC GCA											
TTTTAGGTTTC TCCTTCTTCC TAGATGCCTA TAGGACG TAC AGG TTC GGT GGG CGT											
Met Ser Lys Pro Pro Ala>											
360	365	370	375	380	385	390	395	400			
*	*	*	*	*	*	*	*	*			
CCC AAC CCC ACA CCC CCC CGG AAC CTG GAC TCC CGG ACC TTC ATC ACC											
GGG TTG GGG TGT GGG GGG GCC TTG GAC CTG AGG GCC TGG AAG TAG TGG											
Pro Asn Pro Thr Pro Pro Arg Asn Leu Asp Ser Arg Thr Phe Ile Thr>											
405	410	415	420	425	430	435	440	445	450		
*	*	*	*	*	*	*	*	*	*		
ATT GGA GAC AGA AAC TTT GAG GTG GAG GCT GAT GAC TTG GTG ACC ATC											
TAA CCT CTG TCT TTG AAA CTC CAC CTC CGA CTA CTG AAC CAC TGG TAG											
Ile Gly Asp Arg Asn Phe Glu Val Glu Ala Asp Asp Leu Val Thr Ile>											
455	460	465	470	475	480	485	490	495			
*	*	*	*	*	*	*	*	*			
TCA GAA CTG GGC CGT GGA GCC TAT GGG GTG GTA GAG AAG GTG CGG CAC											
AGT CTT GAC CCG GCA CCT CGG ATA CCC CAC CAT CTC TTC CAC GCC GTG											
Ser Glu Leu Gly Arg Gly Ala Tyr Gly Val Val Glu Lys Val Arg His>											
500	505	510	515	520	525	530	535	540	545		
*	*	*	*	*	*	*	*	*	*		
GCC CAG AGC GGC ACC ATC ATG GCC GTG AAG CGG ATC CGG GCC ACC GTG											
CGG GTC TCG CCG TGG TAG TAC CGG CAC TTC GCC TAG CGG TGG CAC											
Ala Gln Ser Gly Thr Ile Met Ala Val Lys Arg Ile Arg Ala Thr Val>											
550	555	560	565	570	575	580	585	590	595		
*	*	*	*	*	*	*	*	*	*		
AAC TCA CAG GAG CAG AAG CGG CTG CTC ATG GAC CTG GAC ATC AAC ATG											
TTG AGT GTC CTC GTC TTC GCC GAC GAG TAC CTG GAC CTG TAG TTG TAC											
Asn Ser Gln Glu Gln Lys Arg Leu Leu Met Asp Leu Asp Ile Asn Met>											

FIG. 4 - CONT'D

600	605	610	615	620	625	630	635	640
*	*	*	*	*	*	*	*	*
CGC ACG GTC GAC TGT TTC TAC ACT GTC ACC TTC TAC GGG GCA CTA TTC GCG TGC CAG CTG ACA AAG ATG TGA CAG TGG AAG ATG CCC CGT GAT AAG Arg Thr Val Asp Cys Phe Tyr Thr Val Thr Phe Tyr Gly Ala Leu Phe>								
645	650	655	660	665	670	675	680	685
*	*	*	*	*	*	*	*	*
AGA GAG GGA GAC GTG TGG ATC TGC ATG GAG CTC ATG GAC ACA TCC TTG TCT CTC CCT CTG CAC ACC TAG ACG TAC CTC GAG TAC CTG TGT AGG AAC Arg Glu Gly Asp Val Trp Ile Cys Met Glu Leu Met Asp Thr Ser Leu>								
695	700	705	710	715	720	725	730	735
*	*	*	*	*	*	*	*	*
GAC AAG TTC TAC CGG AAG GTG CTG GAT AAA AAC ATG ACA ATT CCA GAG CTG TTC AAG ATG GCC TTC CAC GAC CTA TTT TTG TAC TGT TAA GGT CTC Asp Lys Phe Tyr Arg Lys Val Leu Asp Lys Asn Met Thr Ile Pro Glu>								
740	745	750	755	760	765	770	775	780
*	*	*	*	*	*	*	*	*
GAC ATC CTT GGG GAG ATT GCT GTG TCT ATC GTG CCG GCC CTG GAG CAT CTG TAG GAA CCC CTC TAA CGA CAC AGA TAG CAC GCC CGG GAC CTC GTA Asp Ile Leu Gly Glu Ile Ala Val Ser Ile Val Arg Ala Leu Glu His>								
790	795	800	805	810	815	820	825	830
*	*	*	*	*	*	*	*	*
CTG CAC AGC AAG CTG TCG GTG ATC CAC AGA GAT GTG AAG CCC TCC AAT GAC GTG TCG TTC GAC AGC CAC TAG GTG TCT CTA CAC TTC GGG AGG TTA Leu His Ser Lys Leu Ser Val Ile His Arg Asp Val Lys Pro Ser Asn>								
840	845	850	855	860	865	870	875	880
*	*	*	*	*	*	*	*	*
GTC CTT ATC AAC AAG GAG GGC CAT GTG AAG ATG TGT GAC TTT GGC ATC CAG GAA TAG TTG TTC CTC CCG GTA CAC TTC TAC ACA CTG AAA CCG TAG Val Leu Ile Asn Lys Glu Gly His Val Lys Met Cys Asp Phe Gly Ile>								
885	890	895	900	905	910	915	920	925
*	*	*	*	*	*	*	*	*
AGT GGC TAC TTG GTG GAC TCT GTG GCC AAG ACG ATG GAT GCC GGC TGC TCA CCG ATG AAC CAC CTG AGA CAC CGG TTC TGC TAC CTA CGG CCG ACG Ser Gly Tyr Leu Val Asp Ser Val Ala Lys Thr Met Asp Ala Gly Cys>								
935	940	945	950	955	960	965	970	975
*	*	*	*	*	*	*	*	*
AAG CCC TAC ATG GCC CCT GAG AGG ATC AAC CCA GAG CTG AAC CAG AAG TTC GGG ATG TAC CGG GGA CTC TCC TAG TTG GGT CTC GAC TTG GTC TTC Lys Pro Tyr Met Ala Pro Glu Arg Ile Asn Pro Glu Leu Asn Gln Lys>								
980	985	990	995	1000	1005	1010	1015	1020
*	*	*	*	*	*	*	*	*
GGC TAC AAT GTC AAG TCC GAC GTC TGG AGC CTG GGC ATC ACC ATG ATT CCG ATG TTA CAG TTC AGG CTG CAG ACC TCG GAC CCG TAG TGG TAC TAA Gly Tyr Asn Val Lys Ser Asp Val Trp Ser Leu Gly Ile Thr Met Ile>								
1030	1035	1040	1045	1050	1055	1060	1065	1070
*	*	*	*	*	*	*	*	*
GAG ATG GCC ATC CTG CGG TTC CCT TAC GAG TCC TGG GGG ACC CCG TTC CTC TAC CGG TAG GAC GCC AAG GGA ATG CTC AGG ACC CCC TGG GGC AAG Glu Met Ala Ile Leu Arg Phe Pro Tyr Glu Ser Trp Gly Thr Pro Phe>								
1080	1085	1090	1095	1100	1105	1110	1115	1120

FIG. 4 - CONT'D

CAG CAG CTG AAG CAG GTG GTG GAG GAG CCG TCC CCC CAG CTC CCA GCC
 GTC GTC GAC TTC GTC CAC CAC CTC CTC GGC AGG GGG GTC GAG GGT CGG
 Gln Gln Leu Lys Gln Val Val Glu Glu Pro Ser Pro Gln Leu Pro Ala>

 1125 1130 1135 1140 1145 1150 1155 1160 1165 1170
 * * * * * * * * * *
 GAC CGT TTC TCC CCC GAG TTT GTG GAC TTC ACT GCT CAG TGC CTG AGG
 CTG GCA AAG AGG GGG CTC AAA CAC CTG AAG TGA CGA GTC ACG GAC TCC
 Asp Arg Phe Ser Pro Glu Phe Val Asp Phe Thr Ala Gln Cys Leu Arg>

 1175 1180 1185 1190 1195 1200 1205 1210 1215
 * * * * * * * * *
 AAG AAC CCC GCA GAG CGT ATG AGC TAC CTG GAG CTG ATG GAG CAC CCC
 TTC TTG GGG CGT CTC GCA TAC TCG ATG GAC CTC GAC TAC CTC GTG GGG
 Lys Asn Pro Ala Glu Arg Met Ser Tyr Leu Glu Leu Met Glu His Pro>

 1220 1225 1230 1235 1240 1245 1250 1255 1260 1265
 * * * * * * * * *
 TTC TTC ACC TTG CAC AAA ACC AAG AAG ACG GAC ATT GCT GCC TTC GTG
 AAG AAG TGG AAC GTG TTT TGG TTC TTC TGC CTG TAA CGA CGG AAG CAC.
 Phe Phe Thr Leu His Lys Thr Lys Lys Thr Asp Ile Ala Ala Phe Val>

 1270 1275 1280 1285 1290 1295 1300 1305 1310 1315 1320
 * * * * * * * * * *
 AAG AAG ATC CTG GGA GAA GAC TCA TAGGGCTG GGCCCTCGAC CCCACTCCGG
 TTC TTC TAG GAC CCT CTT CTG AGT ATCCCCGAC CCGGAGCCTG GGGTGAGGCC
 Lys Lys Ile Leu Gly Glu Asp Ser> (SEQ ID NO:2)

 1325 1330 1335 1340 1345 1350 1355 1360 1365 1370 1375 1380
 * * * * * * * * * *
 CCCTCCAGAG CCCCACAGCC CCATCTGGG GGGCAGTGCT CACCCACACC ATAAGCTACT
 GGGAGGTCTC GGGGTGTCGG GGTAGACGCC CCCGTACGA GTGGGTGTGG TATTGATGA

 1385 1390 1395 1400 1405 1410 1415 1420 1425 1430 1435 1440
 * * * * * * * * * *
 GCCATCCTGG CCCAGGGCAT CTGGGAGGAA CCGAGGGGGC TGCTCCCACC TGGCTCTGTG
 CGGTAGGACC GGGTCCCGTA GACCCTCCCT GGCTCCCCCG ACGAGGGTGG ACCGAGACAC

 1445 1450 1455 1460 1465 1470 1475 1480 1485 1490 1495 1500
 * * * * * * * * * *
 GCGAGCCATT TGTCCCAAGT GCCAAAGAAG CAGACCATTG GGGCTCCAG CCAGGCCCTT
 CGCTCGTAA ACAGGGTTCA CGGTTCTTC GTCTGGTAAC CCCGAGGGTC GGTCCGGGAA

 1505 1510 1515 1520 1525 1530 1535 1540 1545 1550 1555 1560
 * * * * * * * * * *
 GTCGGGCCCA CCAGTGCCTC TCCCTGCTGC TCCTAGGACC CGTCCTCCAGC TGCTGAGATC
 CAGCCGGGT GGTACCGGAG AGGGACGACG AGGATCCTGG GCAGAGGTCG ACGACTCTAG

 1565 1570 1575 1580 1585 1590 1595 1600 1605 1610 1615 1620
 * * * * * * * * * *
 CTGGACTGAG GGGGCCTGGA TGCCCCCTGT GGATGCTGCT GCCCCCTGCAC AGCAGGCTGC
 GACCTGACTC CCCCCGGACCT ACGGGGGACA CCTACGACGA CGGGGACGTG TCGTCCGACG

 1625 1630 1635 1640 1645 1650 1655 1660 1665 1670 1675 1680
 * * * * * * * * * *
 CAGTGCCTGG GTGGATGGGC CACCGCCTTG CCCAGCCTGG ATGCCATCCA AGTTGTATAT
 GTCACGGACC CACCTACCCG GTGGCGAAC GGGTCGGACC TACGGTAGGT TCAACATATA

 1685 1690 1695 1700 1705 1710 1715 1720 1725 1730 1735 1740
 * * * * * * * * * *
 TTTTTTAATC TCTCGACTGA ATGGACTTTG CACACTTTGG CCCAGGGTGG CCACACCTCT

FIG. .4 - CONT'D

AAAAAAATTAG AGAGCTGACT TACCTGAAAC GTGTGAAACC GGGTCCCACC GGTGTGGAGA
1745 1750 1755 1760 1765 1770 1775 1780 1785 1790 1795 1800
* * * * * * * * * * * *
ATCCCGGCTT TGGTGCAGGG TACACAAGAG GGGATGAGTT GTGTGAATAC CCCAAGACTC
TAGGGCCGAA ACCACGCCCTC ATGTGTTCTC CCCTACTCAA CACACTTATG GGTTCTGAG
1805 1810 1815 1820 1825 1830 1835 1840 1845 1850 1855 1860
* * * * * * * * * * * *
CCATGAGGGA GATGCCATGA GCCGCCAAG GCCTCCCCCT GGCAGTGGCA AACAGGGCCT
GGTACTCCCT CTACGGTACT CGGCGGGTTC CGGAAGGGGA CGTGACCGT TTGTCCCCGA
1865 1870 1875 1880 1885 1890 1895 1900 1905 1910 1915 1920
* * * * * * * * * * * *
CTGCGGAGCA CACTGGCTCA CCCAGTCCTG CCCGCCACCG TTATCGGTGT CATTCACCTT
GACGCCCTCGT GTGACCGAGT GGGTCAGGAC GGGCGGTGGC AATAGCCACA GTAAGTGGAA
1925 1930 1935 1940 1945 1950 1955 1960 1965 1970 1975 1980
* * * * * * * * * * * *
TCGTGTTTTT TTTAATTAT CCTCTGTTGA TTTTTCTTT TGCTTTATGG GTTTGGCTTG
AGCACAAAAA AAATTAAATA GGAGACAAC AAAAAAGAAA ACGAAATACC CAAACCGAAC
1985 1990 1995 2000 2005 2010 2015 2020 2025 2030
* * * * * * * * * * *
TTTTCTTGC ATGGTTGGA GCTGATCGCT TCTCCCCAC CCCCTAGGGG (SEQ ID NO: 1)
AAAAAGAACG TACCAAACCT CGACTAGCGA AGAGGGGTG GGGGATCCCC

FIG. 5

5	10	15	20	25	30	35	40	45	50	55	60
*	*	*	*	*	*	*	*	*	*	*	*
TAGCTGCAGC ACAGCCTTCC CTAACGTTGC AACTGGGGGA AAAATCACTT TCCAGTCTGT											
ATCGACGTCG TGTGGAAAGG GATTGCAACG TTGACCCCCCT TTTTAGTGAA AGGTCAGACA											
65	70	75	80	85	90	95	100	105	110	115	120
*	*	*	*	*	*	*	*	*	*	*	*
TTTGCAAGGT GTGCATTTCC ATCTTGATTTC CCTGAAAGTC CATCTGCTGC ATCGGTCAAG											
AACACGTTCCA CACGTAAGG TAGAACTAAG GGACTTTCAAG GTAGACGACG TAGCCAGTT											
125	130	135	140	145	150	155	160	165	170	175	180
*	*	*	*	*	*	*	*	*	*	*	*
AGAAAATCCA CTTGCATGAA GATTGCACGC CTGCAGCTTG CATCTTTGTT GCAAAACTAG											
TCTTTGAGGT GAACGTAATT CTAACGTCG GACGTCGAAC GTAGAAACAA CGTTTGATC											
185	190	195	200	205	210	215	220	225	230	235	240
*	*	*	*	*	*	*	*	*	*	*	*
CTACAGAAGA GAAGCAAGGC AAAGTCTTTT GTGCTCCCT CCCCATCAA AGGAAAGGGG											
GATGTCCTCT CTTCGTTCCG TTTCAGAAAA CACGAGGGGA GGGGGTAGTT TCCTTTCC											
245	250	255	260	265	270	275	280	285			
*	*	*	*	*	*	*	*				
AAA ATG TCT CAG TCG AAA GGC AAG AAG CGA AAC CCT GGC CTT AAA ATT											
TTT TAC AGA GTC AGC TTT CCG TTC TTC GCT TTG GGA CCG GAA TTT TAA											
Met Ser Gln Ser Lys Gly Lys Lys Arg Asn Pro Gly Leu Lys Ile>											
290	295	300	305	310	315	320	325	330	335		
*	*	*	*	*	*	*	*	*			
CCA AAA GAA GCA TTT GAA CAA CCT CAG ACC AGT TCC ACA CCA CCT AGA											
GGT TTT CTT CGT AAA CTT GTT GGA GTC TGG TCA AGG TGT GGT GGA TCT											
Pro Lys Glu Ala Phe Glu Gln Pro Gln Thr Ser Ser Thr Pro Pro Arg>											
340	345	350	355	360	365	370	375	380			
*	*	*	*	*	*	*	*				
GAT TTA GAC TCC AAG GCT TGC ATT TCT ATT GGA AAT CAG AAC TTT GAG											
CTA AAT CTG AGG TTC CGA ACG TAA AGA TAA CCT TTA GTC TTG AAA CTC											
Asp Leu Asp Ser Lys Ala Cys Ile Ser Ile Gly Asn Gln Asn Phe Glu>											
385	390	395	400	405	410	415	420	425	430		
*	*	*	*	*	*	*	*	*	*		
GTG AAG GCA GAT GAC CTG GAG CCT ATA ATG GAA CTG GGA CGA GGT GCG											
CAC TTC CGT CTA CTG GAC CTC GGA TAT TAC CTT GAC CCT GCT CCA CGC											
Val Lys Ala Asp Asp Leu Glu Pro Ile Met Glu Leu Gly Arg Gly Ala>											
435	440	445	450	455	460	465	470	475	480		
*	*	*	*	*	*	*	*	*	*		
TAC GGG GTG GTG GAG AAG ATG CGG CAC GTG CCC AGC GGG CAG ATC ATG											
ATG CCC CAC CAC CTC TTC TAC GCC GTG CAC GGG TCG CCC GTC TAG TAC											
Tyr Gly Val Val Glu Lys Met Arg His Val Pro Ser Gly Gln Ile Met>											
485	490	495	500	505	510	515	520	525			
*	*	*	*	*	*	*	*				
GCA GTG AAG CGG ATC CGA GCC ACA GTA AAT AGC CAG GAA CAG AAA CGG											
CGT CAC TTC GCC TAG GCT CGG TGT CAT TTA TCG GTC CTT GTC TTT GCC											
Ala Val Lys Arg Ile Arg Ala Thr Val Asn Ser Gln Glu Gln Lys Arg>											
530	535	540	545	550	555	560	565	570	575		
*	*	*	*	*	*	*	*	*			
CTA CTG ATG GAT TTG GAT ATT TCC ATG AGG ACG GTG GAC TGT CCA TTC											
GAT GAC TAC CTA AAC CTA TAA AGG TAC TCC TGC CAC CTG ACA GGT AAG											

FIG. 5 - CONT'D

Leu Leu Met Asp Leu Asp Ile Ser Met Arg Thr Val Asp Cys Pro Phe>

580 585 590 595 600 605 610 615 620

* * * * * * * * * *

ACT GTC ACC TTT TAT GGC GCA CTG TTT CGG GAG GGT GAT GTG TGG ATC
TGA CAG TGG AAA ATA CCG CGT GAC AAA GCC CTC CCA CTA CAC ACC TAG
Thr Val Thr Phe Tyr Gly Ala Leu Phe Arg Glu Gly Asp Val Trp Ile>

625 630 635 640 645 650 655 660 665 670

* * * * * * * * * *

TGC ATG GAG CTC ATG GAT ACA TCA CTA GAT AAA TTC TAC AAA CAA GTT
ACG TAC CTC GAG TAC CTA TGT AGT GAT CTA TTT AAG ATG TTT GTT CAA
Cys Met Glu Leu Met Asp Thr Ser Leu Asp Lys Phe Tyr Lys Gln Val>

675 680 685 690 695 700 705 710 715 720

* * * * * * * * * *

ATT GAT AAA GGC CAG ACA ATT CCA GAG GAC ATC TTA GGG AAA ATA GCA
TAA CTA TTT CCG GTC TGT TAA GGT CTC CTG TAG AAT CCC TTT TAT CGT
Ile Asp Lys Gly Gln Thr Ile Pro Glu Asp Ile Leu Gly Lys Ile Ala>

725 730 735 740 745 750 755 760 765

* * * * * * * * * *

GTT TCT ATT GTA AAA GCA TTA GAA CAT TTA CAT AGT AAG CTG TCT GTC
CAA AGA TAA CAT TTT CGT AAT CTT GTA AAT GTA TCA TTC GAC AGA CAG
Val Ser Ile Val Lys Ala Leu Glu His Leu His Ser Lys Leu Ser Val>

770 775 780 785 790 795 800 805 810 815

* * * * * * * * * *

ATT CAC AGA GAC GTC AAG CCT TCT AAT GTA CTC ATC AAT GCT CTC GGT
TAA GTG TCT CTG CAG TTC GGA AGA TTA CAT GAG TAG TTA CGA GAG CCA
Ile His Arg Asp Val Lys Pro Ser Asn Val Leu Ile Asn Ala Leu Gly>

820 825 830 835 840 845 850 855 860

* * * * * * * * * *

CAA GTG AAG ATG TGC GAT TTT GGA ATC AGT GGC TAC TTG GTG GAC TCT
GTT CAC TTC TAC ACG CTA AAA CCT TAG TCA CCG ATG AAC CAC CTG AGA
Gln Val Lys Met Cys Asp Phe Gly Ile Ser Gly Tyr Leu Val Asp Ser>

865 870 875 880 885 890 895 900 905 910

* * * * * * * * * *

GTT GCT AAA ACA ATT GAT GCA GGT TGC AAA CCA TAC ATG GCC CCT GAA
CAA CGA TTT TGT TAA CTA CGT CCA ACG TTT GGT ATG TAC CGG GGA CTT
Val Ala Lys Thr Ile Asp Ala Gly Cys Lys Pro Tyr Met Ala Pro Glu>

915 920 925 930 935 940 945 950 955 960

* * * * * * * * * *

AGA ATA AAC CCA GAG CTC AAC CAG AAG GGA TAC AGT GTG AAG TCT GAC
TCT TAT TTG GGT CTC GAG TTG GTC TTC CCT ATG TCA CAC TTC AGA CTG
Arg Ile Asn Pro Glu Leu Asn Gln Lys Gly Tyr Ser Val Lys Ser Asp>

965 970 975 980 985 990 995 1000 1005

* * * * * * * * * *

ATT TGG AGT CTG GGC ATC ACG ATG ATT GAG TTG GCC ATC CTT CGA TTT
TAA ACC TCA GAC CCG TAG TGC TAC TAA CTC AAC CGG TAG GAA GCT AAA
Ile Trp Ser Leu Gly Ile Thr Met Ile Glu Leu Ala Ile Leu Arg Phe>

1010 1015 1020 1025 1030 1035 1040 1045 1050 1055

* * * * * * * * * *

CCC TAT GAT TCA TGG GGA ACT CCA TTT CAG CAG CTC AAA CAG GTG GTA
GGG ATA CTA AGT ACC CCT TGA GGT AAA GTC GTC GAG TTT GTC CAC CAT
Pro Tyr Asp Ser Trp Gly Thr Pro Phe Gln Gln Leu Lys Gln Val Val>

FIG. 5 - CONT'D

1060 1065 1070 1075 1080 1085 1090 1095 1100
 * * * * * * * * * *
 GAG GAG CCA TCG CCA CAA CTC CCA GCA GAC AAG TTC TCT GCA GAG TTT
 CTC CTC GGT AGC GGT GTT GAG GGT CGT CTG TTC AAG AGA CGT CTC AAA
 Glu Glu Pro Ser Pro Gln Leu Pro Ala Asp Lys Phe Ser Ala Glu Phe>

 1105 1110 1115 1120 1125 1130 1135 1140 1145 1150
 * * * * * * * * * *
 GTT GAC TTT ACC TCA CAG TGC TTA AAG AAG AAT TCC AAA GAA CGG CCT
 CAA CTG AAA TGG AGT GTC ACG AAT TTC TTC TTA AGG TTT CTT GCC GGA
 Val Asp Phe Thr Ser Gln Cys Leu Lys Lys Asn Ser Lys Glu Arg Pro>

 1155 1160 1165 1170 1175 1180 1185 1190 1195 1200
 * * * * * * * * * *
 ACA TAC CCA GAG CTA ATG CAA CAT CCA TTT TTC ACC CTA CAT GAA TCC
 TGT ATG GGT CTC GAT TAC GTT GTA GGT AAA AAG TGG GAT GTA CTT AGG
 Thr Tyr Pro Glu Leu Met Gln His Pro Phe Phe Thr Leu His Glu Ser>

 1205 1210 1215 1220 1225 1230 1235 1240 1245 1250
 * * * * * * * * * *
 AAA GGA ACA GAT GTG GCA TCT TTT GTA AAA CTG ATT CTT GGA GAC TAAAAA
 TTT CCT TGT CTA CAC CGT AGA AAA CAT TTT GAC TAA GAA CCT CTG ATTTT
 Lys Gly Thr Asp Val Ala Ser Phe Val Lys Leu Ile Leu Gly Asp> (SEQ ID NO:4)

 1255 1260 1265 1270 1275 1280 1285 1290 1295 1300 1305 1310
 * * * * * * * * * *
 ACCAGTGGAC TTAATCGGTT GACCCTACTG TGGATTGGTG GGTTTCGGGG TGAAGCAAGT
 TCGTCACCTG AATTAGCCAA CTGGGATGAC ACCTAACAC CCAAAGCCCC ACTTCGTCA

 1315 1320 1325 1330 1335 1340 1345 1350 1355 1360 1365 1370
 * * * * * * * * * *
 TCACTACAGC ATCAATAGAA AGTCATCTTT GAGATAATT AACCCCTGCCT CTCAGAGGGT
 AGTGATGTCG TAGTTATCTT TCAGTAGAAA CTCTATTAAA TTGGGACGGA GAGTCTCCC

 1375 1380 1385 1390 1395 1400 1405 1410 1415 1420 1425 1430
 * * * * * * * * * *
 TTTCTCTCCC AATTTCTTT TTACTCCCCC TCTTAAGGGG GCCCTTGAAT CTATAGTATA
 AAAGAGAGGG TTAAAAGAAA AATGAGGGGG AGAATTCCCC CGGAACCTTA GATATCATAT

 1435 1440 1445 1450 1455 1460 1465 1470 1475 1480 1485 1490
 * * * * * * * * * *
 GAATGAACTG TCTAGATGGA TGAATTATGA TAAAGGCTTA GGACTTCAAA AGGTGATTAA
 CTTACTTGAC AGATCTACCT ACTTAATACT ATTTCCGAAT CCTGAAGTTT TCCACTAATT

 1495 1500 1505 1510 1515 1520 1525 1530 1535 1540 1545 1550
 * * * * * * * * * *
 ATATTTAATG ATGTGTCTA TGAGTCCTCA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
 TATAAATTAC TACACAGTAT ACTCAGGAGT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT

 1555 1560 1565 1570 1575 1580 1585 1590 1595 1600
 * * * * * * * * * *
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA (SEQ ID NO:3)
 TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TT

FIG. 6

5	10	15	20	25	30	35	40	45	50	55
*	*	*	*	*	*	*	*	*	*	*
CTAGGGTCCC CGGCGCCAGG CCACCCGGCC GTCAGCAGC ATG CAG GGT AAA CGC AAA GATCCCAGGG GCCGCGGTCC GGTGGGCCGG CAGTCGTG TAC GTC CCA TTT GCG TTT Met Gln Gly Lys Arg Lys>										
60	65	70	75	80	85	90	95	100	105	*
*	*	*	*	*	*	*	*	*	*	*
GCA CTG AAG TTG AAT TTT GCA AAT CCA CCT TTC AAA TCT ACA GCA AGG CGT GAC TTC AAC TTA AAA CGT TTA GGT GGA AAG TTT AGA TGT CGT TCC Ala Leu Lys Leu Asn Phe Ala Asn Pro Pro Phe Lys Ser Thr Ala Arg>										
110	115	120	125	130	135	140	145	150	*	*
*	*	*	*	*	*	*	*	*	*	*
TTT ACT CTG AAT CCC AAT CCT ACA GGA GTT CAA AAC CCA CAC ATA GAG AAA TGA GAC TTA GGG TTA GGA TGT CCT CAA GTT TTG GGT GTG TAT CTC Phe Thr Leu Asn Pro Asn Pro Thr Gly Val Gln Asn Pro His Ile Glu>										
155	160	165	170	175	180	185	190	195	200	*
*	*	*	*	*	*	*	*	*	*	*
AGA CTG AGA ACA CAC AGC ATT GAG TCA TCA GGA AAA CTG AAG ATC TCC TCT GAC TCT TGT GTG TCG TAA CTC AGT AGT CCT TTT GAC TTC TAG AGG Arg Leu Arg Thr His Ser Ile Glu Ser Ser Gly Lys Leu Lys Ile Ser>										
205	210	215	220	225	230	235	240	245	*	*
*	*	*	*	*	*	*	*	*	*	*
CCT GAA CAA CAC TGG GAT TTC ACT GCA GAG GAC TTG AAA GAC CTT GGA GGA CTT GTT GTG ACC CTA AAG TGA CGT CTC CTG AAC TTT CTG GAA CCT Pro Glu Gln His Trp Asp Phe Thr Ala Glu Asp Leu Lys Asp Leu Gly>										
250	255	260	265	270	275	280	285	290	295	*
*	*	*	*	*	*	*	*	*	*	*
GAA ATT GGA CGA GGA GCT TAT GGT TCT GTC AAC AAA ATG GTC CAC AAA CTT TAA CCT GCT CCT CGA ATA CCA AGA CAG TTG TTT TAC CAG GTG TTT Glu Ile Gly Arg Gly Ala Tyr Gly Ser Val Asn Lys Met Val His Lys>										
300	305	310	315	320	325	330	335	340	345	*
*	*	*	*	*	*	*	*	*	*	*
CCA AGT GGG CAA ATA ATG GCA GTT AAA AGA ATT CGG TCA ACA GTG GAT GGT TCA CCC GTT TAT TAC CGT CAA TTT TCT TAA GCC AGT TGT CAC CTA Pro Ser Gly Gln Ile Met Ala Val Lys Arg Ile Arg Ser Thr Val Asp>										
350	355	360	365	370	375	380	385	390	*	*
*	*	*	*	*	*	*	*	*	*	*
GAA AAA GAA CAA AAA CAA CTT CTT ATG GAT TTG GAT GTA GTA ATG CGG CTT TTT CTT GTT TTT GTT GAA GAA TAC CTA AAC CTA CAT CAT TAC GCC Glu Lys Glu Gln Lys Glu Leu Leu Met Asp Leu Asp Val Val Met Arg>										
395	400	405	410	415	420	425	430	435	440	*
*	*	*	*	*	*	*	*	*	*	*
AGT AGT GAT TGC CCA TAC ATT GTT CAG TTT TAT GGT GCA CTC TTC AGA TCA TCA CTA ACG GGT ATG TAA CAA GTC AAA ATA CCA CGT GAG AAG TCT Ser Ser Asp Cys Pro Tyr Ile Val Gln Phe Tyr Gly Ala Leu Phe Arg>										
445	450	455	460	465	470	475	480	485	*	*
*	*	*	*	*	*	*	*	*	*	*
GAG GGT GAC TGT TGG ATC TGT ATG GAA CTC ATG TCT ACC TCG TTT GAT CTC CCA CTG ACA ACC TAG ACA TAC CTT GAG TAC AGA TGG AGC AAA CTA Glu Gly Asp Cys Trp Ile Cys Met Glu Leu Met Ser Thr Ser Phe Asp>										

FIG. 6 - CONT'D

490 495 500 505 510 515 520 525 530 535
 * * * * * * * * * *
 AAG TTT TAC AAA TAT GTA TAT AGT GTA TTA GAT GAT GTT ATT CCA GAA
 TTC AAA ATG TTT ATA CAT ATA TCA CAT AAT CTA CTA CAA TAA GGT CTT
 Lys Phe Tyr Lys Tyr Val Tyr Ser Val Leu Asp Asp Val Ile Pro Glu>

 540 545 550 555 560 565 570 575 580 585
 * * * * * * * * * *
 GAA ATT TTA GGC AAA ATC ACT TTA GCA ACT GTG AAA GCA CTA AAC CAC
 CTT TAA AAT CCG TTT TAG TGA AAT CGT TGA CAC TTT CGT GAT TTG GTG
 Glu Ile Leu Gly Lys Ile Thr Leu Ala Thr Val Lys Ala Leu Asn His>

 590 595 600 605 610 615 620 625 630
 * * * * * * * * * *
 TTA AAA GAA AAC TTG AAA ATT ATT CAC AGA GAT ATC AAA CCT TCC AAT
 AAT TTT CTT TTG AAC TTT TAA TAA GTG TCT CTA TAG TTT GGA AGG TTA
 Leu Lys Glu Asn Leu Lys Ile Ile His Arg Asp Ile Lys Pro Ser Asn>

 635 640 645 650 655 660 665 670 675 680
 * * * * * * * * * *
 ATT CTT CTG GAC AGA AGT GGA AAT ATT AAG CTC TGT GAC TTC GGC ATC.
 TAA GAA GAC CTG TCT TCA CCT TTA TAA TTC GAG ACA CTG AAG CCG TAG
 Ile Leu Leu Asp Arg Ser Gly Asn Ile Lys Leu Cys Asp Phe Gly Ile>

 685 690 695 700 705 710 715 720 725
 * * * * * * * * * *
 AGT GGA CAG CTT GTG GAC TCT ATT GCC AAG ACA AGA GAT GCT GGC TGT
 TCA CCT GTC GAA CAC CTG AGA TAA CGG TTC TGT TCT CTA CGA CCG ACA
 Ser Gly Gln Leu Val Asp Ser Ile Ala Lys Thr Arg Asp Ala Gly Cys>

 730 735 740 745 750 755 760 765 770 775
 * * * * * * * * * *
 AGG CCA TAC ATG GCA CCT GAA AGA ATA GAC CCA AGC GCA TCA CGA CAA
 TCC GGT ATG TAC CGT GGA CTT TCT TAT CTG GGT TCG CGT AGT GCT GTT
 Arg Pro Tyr Met Ala Pro Glu Arg Ile Asp Pro Ser Ala Ser Arg Gln>

 780 785 790 795 800 805 810 815 820 825
 * * * * * * * * * *
 GGA TAT GAT GTC CGC TCT GAT GTC TGG AGT TTG GGG ATC ACA TTG TAT
 CCT ATA CTA CAG GCG AGA CTA CAG ACC TCA AAC CCC TAG TGT AAC ATA
 Gly Tyr Asp Val Arg Ser Asp Val Trp Ser Leu Gly Ile Thr Leu Tyr>

 830 835 840 845 850 855 860 865 870
 * * * * * * * * * *
 GAG TTG GCC ACA GGC CGA TTT CCT TAT CCA AAG TGG AAT AGT GTA TTT
 CTC AAC CGG TGT CCG GCT AAA GGA ATA GGT TTC ACC TTA TCA CAT AAA
 Glu Leu Ala Thr Gly Arg Phe Pro Tyr Pro Lys Trp Asn Ser Val Phe>

 875 880 885 890 895 900 905 910 915 920
 * * * * * * * * * *
 GAT CAA CTA ACA CAA GTC GTG AAA GGA GAT CCT CCG CAG CTG AGT AAT
 CTA GTT GAT TGT GTT CAG CAC TTT CCT CTA GGA GGC GTC GAC TCA TTA
 Asp Gln Leu Thr Gln Val Val Lys Gly Asp Pro Pro Gln Leu Ser Asn>

 925 930 935 940 945 950 955 960 965
 * * * * * * * * * *
 TCT GAG GAA AGG GAA TTC TCC CCG AGT TTC ATC AAC TTT GTC AAC TTG
 AGA CTC CTT TCC CTT AAG AGG GGC TCA AAG TAG TTG AAA CAG TTG AAC
 Ser Glu Glu Arg Glu Phe Ser Pro Ser Phe Ile Asn Phe Val Asn Leu>

 970 975 980 985 990 995 1000 1005 1010 1015
 * * * * * * * * * *

FIG. 6 - CONT'D

TGC CTT ACG AAG GAT GAA TCC AAA AGG CCA AAG TAT AAA GAG CTT CTG
 ACG GAA TGC TTC CTA CTT AGG TTT TCC GGT TTC ATA TTT CTC GAA GAC
 Cys Leu Thr Lys Asp Glu Ser Lys Arg Pro Lys Tyr Lys Glu Leu Leu>

1020 1025 1030 1035 1040 1045 1050 1055 1060 1065

* * * * * * * * * *
 AAA CAT CCC TTT ATT TTG ATG TAT GAA GAA CGT GCC GTT GAG GTC GCA
 TTT GTA GGG AAA TAA AAC TAC ATA CTT CTT GCA CGG CAA CTC CAG CGT
 Lys His Pro Phe Ile Leu Met Tyr Glu Glu Arg Ala Val Glu Val Ala>

1070 1075 1080 1085 1090 1095 1100 1105 1110

* * * * * * * * * *
 TGC TAT GTT TGT AAA ATC CTG GAT CAA ATG CCA GCT ACT CCC AGC TCT
 ACG ATA CAA ACA TTT TAG GAC CTA GTT TAC GGT CGA TGA GGG TCG AGA
 Cys Tyr Val Cys Lys Ile Leu Asp Gln Met Pro Ala Thr Pro Ser Ser>

1115 1120 1125 1130 1135 1140 1145 1150 1155 1160 1165 1170

* * * * * * * * * *
 CCC ATG TAT GTC GAT TG ATATCGYTGC TACATCAGAC TCTAGAAAAA AGGGCTGAGA
 GGG TAC ATA CAG CTA AC TATAGCRACG ATGTAGTCTG AGATCTTTT TCCCGACTCT
 Pro Met Tyr Val Asp> (SEQ ID NO:6)

1175 1180 1185 1190 1195 1200 1205 1210 1215 1220 1225 1230

* * * * * * * * * *
 GGAAGCAAGA CGTAAAGAAC TTTCATCCCG TATCACAGTG TTTTTATTGC TCGCCCAGAC
 CCTTCGTTCT GCATTTCTTA AAAGTAGGGC ATAGTGTACAC AAAAATAACG AGCGGGTCTG

1235 1240 1245 1250 1255 1260 1265 1270 1275 1280 1285 1290

* * * * * * * * * *
 ACCATGTGCA ATAAGATTGG TGTCGTTTC CATCATGTCT GTATACTCCT GTCACCTAGA
 TGGTACACGT TATTCTAACCAACAG GTAGTACAGA CATATGAGGA CAGTGGATCT

1295 1300 1305 1310 1315 1320 1325 1330 1335 1340 1345 1350

* * * * * * * * * *
 ACGTGCATCC TTGTAATACC TGATTGATCA CACAGTGTAA GTGCTGGTCA GAGAGACCTC
 TGCACGTAGG AACATTATGG ACTAACTAGT GTGTCACAAT CACGACCAAGT CTCTCTGGAG

1355 1360 1365 1370 1375 1380 1385 1390 1395 1400 1405 1410

* * * * * * * * * *
 ATCCTGCTCT TTTGTGATGA ACATATTCTAT GAAATGTGGA AGTCAGTACG ATCAAGTTGT
 TAGGACGAGA AAACACTACT TGTATAAGTA CTTTACACCT TCAGTCATGC TAGTTCAACA

1415 1420 1425 1430 1435 1440 1445 1450 1455 1460 1465 1470

* * * * * * * * * *
 TGACTGTGAT TAGATCACAT CTTAAATTCA TTTCTAGACT CAAAACCTGG AGATGCAGCT
 ACTGACACTA ATCTAGTGTAA GAATTTAAGT AAAGATCTGA GTTTGGACC TCTACGTCGA

1475 1480 1485 1490 1495 1500 1505 1510 1515 1520 1525 1530

* * * * * * * * * *
 ACTGGAATGG TGTGTTGTC GACTTCCAAA TCCTGGAGG ACACAGTGAT GAATGTACTA
 TGACCTTACCA CACAAACAGT CTGAAGGTTC AGGACCTTCC TGTGTCACTA CTTACATGAT

1535 1540 1545 1550 1555 1560 1565 1570 1575 1580 1585 1590

* * * * * * * * * *
 TATCTGAACA TAGAAAATCG GGCTTGAGTG AGAAGAGCTT GCACAGCCAA CGAGACACAT
 ATAGACTTGT ATCTTGTGAGC CCGAACTCAC TCTTCTCGAA CGTGTGGTT GCTCTGTGTA

1595 1600 1605 1610 1615 1620 1625 1630 1635 1640 1645 1650

* * * * * * * * * *
 TGCCTTCTGG AGCTGGGAGA CAAAGGAGGA ATTTACTTTC TTCACCAAGT GCAATAGATT
 ACGGAAGACC TCGACCCCTCT GTTCCCTCCT TAAATGAAAG AAGTGGTTCA CGTTATCTAA

FIG. 6 - CONT'D

1655 1660 1665 1670 1675 1680 1685 1690 1695 1700 1705 1710
 * * * * * * * * * * * *
 ACTGATGTGA TATTCTGTTG CTTTACAGTT ACAGTTGATG TTTGGGGATC GATGTGCTCA
 TGACTACACT ATAAGACAAC GAAATGTCAA TGTCAACTAC AAACCCCTAG CTACACGGAGT

 1715 1720 1725 1730 1735 1740 1745 1750 1755 1760 1765 1770
 * * * * * * * * * * * *
 GCCAAATTTCTGTTGAAA TATCATGTTA AATTAGAACGTT AATTATCTT TACCAAAAAC
 CGGTTTAAAG GACAAACTTT ATAGTACAAT TTAATCTTAC TAAATAGAA ATGGTTTTG

 1775 1780 1785 1790 1795 1800 1805 1810 1815 1820 1825 1830
 * * * * * * * * * * * *
 CATGTTGCGT TCAAAGAGGT GAACATTAAA ATATAGAGAC AGGACAGAAT GTGTTCTTT
 GTACAACGCA AGTTTCTCCA TTGTAATT TATATCTCTG TCCTGTCCTA CACAAGAAAA

 1835 1840 1845 1850 1855 1860 1865 1870 1875 1880 1885 1890
 * * * * * * * * * * * *
 CTCCCTCTACC AGTCCTATTT TTCAATGGGA AGACTCAGGA GTCTGCCACT TGTCAAAGAA
 GAGGAGATGG TCAGGATAAA AAGTTACCCCT TCTGAGTCCT CAGACGGTGA ACAGTTCTT

 1895 1900 1905 1910 1915 1920 1925 1930 1935 1940 1945 1950
 * * * * * * * * * * * *
 GGTGCTGATC CTAAGAATTT TTCAATTCTCA GAATTGGTG TGCTGCCAAC TTGATGTTCC
 CCACGACTAG GATTCTTAAA AAGTAAGAGT CTTAAGCCAC ACGACGGTTG AACTACAAGG

 1955 1960 1965 1970 1975 1980 1985 1990 1995 2000 2005 2010
 * * * * * * * * * * * *
 ACCTGCCACA AACCACCAAGG ACTGAAAGAA GAAAACAGTA CAGAAGGCAA AGTTTACAGA
 TGGACGGTGT TTGGTGGTCC TGACTTTCTT CTTTGTCT GTCTTCGGT TCAAATGTCT

 2015 2020 2025 2030 2035 2040 2045 2050 2055 2060 2065 2070
 * * * * * * * * * * * *
 TGTGTTTAAT TCTAGTATTT TATCTGGAAC AACTTGTAGC AGCTATATAT TTCCCCCTGG
 ACAAAAATTA AGATCATAAA ATAGACCTTG TTGAACATCG TCGATATATA AAGGGGAACC

 2075 2080 2085 2090 2095 2100 2105 2110 2115 2120 2125 2130
 * * * * * * * * * * * *
 TCCCAAGCCT GATACTTTAG CCATCATAAC TCACTAACAG GGAGAAGTAG CTAGTAGCAA
 AGGGTTCGGA CTATGAAATC GGTAGTATTG AGTGTATTG CCTCTTCATC GATCATCGTT

 2135 2140 2145 2150 2155 2160 2165 2170 2175 2180 2185 2190
 * * * * * * * * * * * *
 TGTGCTTGA TTGATTAGAT AAAGATTTCT AGTAGGCAGC AAAAGACCAA ATCTCAGTTG
 ACACGGAAC AACTAATCTA TTCTAAAGA TCATCCGTCG TTTCTGGTT TAGAGTCAAC

 2195 2200 2205 2210 2215 2220 2225 2230 2235 2240 2245 2250
 * * * * * * * * * * * *
 TTTGCTTCTT GCCATCACTG GTCCAGGTCT TCAGTTCCG AATCTCTTTC CCTTCCCCGT
 AACGAAGAA CGGTAGTGAC CAGGTCCAGA AGTCAAAGGC TTAGAGAAAG GGAAGGGGAC

 2255 2260 2265 2270 2275 2280 2285 2290 2295 2300 2305 2310
 * * * * * * * * * * * *
 TGGCTATGIG TCGCTATGIG ACTTGCGCTT AATCCAATAT TTTGCTTCTT TTCTATATCA
 ACCAGATAAC AGCGATAACAC TGAACGCGAA TTAGGTTATA AAACGGAAAA AAGATATAGT

 2315 2320 2325 2330 2335 2340 2345 2350 2355 2360 2365 2370
 * * * * * * * * * * * *
 AAAAACCTTT ACAGTTAGCA GGGATGTTCC TTACCGAGGA TTTTTAACCC CCAATCTCTC
 TTTTGGAAA TGTCAATCGT CCCTACAAGG AATGGCTCCT AAAAATGGG GGTTAGAGAG

 2375 2380 2385 2390 2395 2400 2405 2410 2415 2420 2425 2430
 * * * * * * * * * * * *

FIG. 6 - CONT'D

ATAATCGCTA GTGTTAAAAA GGCTAAGAAT AGTGGGCC AACCGATGTG GTAGGTGATA
TATTAGCGAT CACAAATTTT CCGATTCTTA TCACCCCGGG TTGGCTACAC CATCCACTAT

2435 2440 2445 2450 2455 2460 2465 2470 2475 2480 2485 2490
* * * * * * * * * * * *
AAGAGGCATC TTTCTAGAG ACACATTGGA CCAGATGAGG ATCCGAAACG GCAGCCTTTA
TTCTCCGTAG AAAAGATCTC TGTGTAACCT GGTCTACTCC TAGGCTTTGC CGTCGGAAAT

2495 2500 2505 2510 2515 2520 2525 2530 2535 2540 2545 2550
* * * * * * * * * * * *
CGTCATCAC CTGCTAGAAC CTCTCGTAGT CCATCACCAT TTCTTGGCAT TGGAATTCTA
GCAAGTAGTG GACGATCTTG GAGAGCATCA GGTAGTGGTA AAGAACCGTA ACCTTAAGAT

2555 2560 2565 2570 2575 2580 2585 2590 2595 2600 2605 2610
* * * * * * * * * * * *
CTGGAAAAAA ATACAAAAAG CAAAACAAAA CCCTCAGCAC TGTACAAGA GGCCATTAA
GACCTTTTTT TATGTTTTTC GTTTTGTTTT GGGAGTCGTG ACAATGTTCT CCGTAAATT

2615 2620 2625 2630 2635 2640 2645 2650 2655 2660 2665 2670
* * * * * * * * * * * *
GTATCTTGTG CTTCTTCACT TACCCATTAG CCAGGTTCTC ATTAGTTTTT GCTTGGCCCT
CATAGAACAC GAAGAAGTGA ATGGTAATC GGTCCAAGAG TAATCCAAA CGAACCCGGA

2675 2680 2685 2690 2695 2700 2705 2710 2715 2720 2725 2730
* * * * * * * * * * * *
CCCTGGCACT GAACCTTAGG CTTTGTATGA CAGTGAAGCA GCACTGTGAG TGGTTCAAGC
GGGACCGTGA CTTGGAATCC GAAACATACT GTCACCTCGT CGTGACACTC ACCAAGTCG

2735 2740 2745 2750 2755 2760 2765 2770 2775 2780 2785 2790
* * * * * * * * * * * *
ACACTGGAAT ATAAAACAGT CATGGCTGA GATGCAGGTG ATGCCATTAC AGAACCAAAT
TGTGACCTTA TATTTTGTCA GTACCGGACT CTACGTCCAC TACGGTAATG TCTTGGTTA

2795 2800 2805 2810 2815 2820 2825 2830 2835 2840 2845 2850
* * * * * * * * * * * *
CGTGGCACGT ATTGCTGTGT CTCTCTCAG AGTGACAGTC ATAAATACTG TCAAACATA
GCACCGTGA TAACGACACA GAGGAGAGTC TCACTGTCAG TATTTATGAC AGTTTGTAT

2855 2860 2865 2870 2875 2880 2885 2890 2895 2900 2905 2910
* * * * * * * * * * * *
AAGGGAGAAT GGTGCTGTTT AAAGTCACAT CCCTGTAAAT TGCAGAATTG AAAAGTGATT
TTCCCTCTTA CCACGACAAA TTTCAGTGTG GGGACATTAA ACGTCTTAAG TTTTCACTAA

2915 2920 2925 2930 2935 2940 2945 2950 2955 2960 2965 2970
* * * * * * * * * * * *
ATCTCTTGA TCTACTTGCC TCATTTCCCT ATCTCTCCC CCACGGTATC CTAAACTTTA
TAGAGAAACT AGATGAACGG AGTAAGGGG TAGAAGAGGG GGTGCCATAG GATTTGAAAT

2975 2980 2985 2990 2995 3000 3005 3010 3015 3020 3025 3030
* * * * * * * * * * * *
GACTCCCCAC TGTCTGAAA GGAGACATTG CTCTATGTCT GCCTTCGACC ACAGCAAGCC
CTGAAGGGTG ACAAGACTTT CCTCTGTAAAC GAGATACAGA CGGAAGCTGG TGTCGTTCGG

3035 3040 3045 3050 3055 3060 3065 3070 3075 3080 3085 3090
* * * * * * * * * * * *
ATCATCCTCC ATTGCTCCCG GGGACTCAAG AGGAATCTGT TTCTCTGCTG TCAACTTCCC
TAGTAGGAGG TAACGAGGGC CCCTGAGTTC TCCTTAGACA AAGAGACGAC AGTTGAAGGG

3095 3100 3105 3110 3115 3120 3125 3130 3135 3140 3145 3150
* * * * * * * * * * * *
ATCTGGCTCA GCATAGGGTC ACTTTGCCAT TATGCAAATG GAGATAAAAG CAATTCTGGC
TAGACCGAGT CGTATCCCAG TGAAACGGTA ATACGTTAC CTCTATTTC GTTAAGACCG

FIG. 6 - CONT'D

3155 3160 3165 3170 3175 3180 3185 3190 3195 3200 3205 3210
* * * * * * * * * * * *
TGTCCAGGAG CTAATCTGAC CGTTCTATTG TGTGGATGAC CACATAAGAA GGCAATTAA
ACAGGTCTC GATTAGACTG GCAAGATAAC ACACCTACTG GTGTATTCTT CCGTTAAAAT
3215 3220 3225 3230 3235 3240 3245 3250 3255 3260 3265 3270
* * * * * * * * * * * *
GTGTATTAAT CATAGATTAT TATAAACTAT AAACCTAAGG GCAAGGAGTT TATTACAATG
CACATAATTA GTATCTAATA ATATTGATA TTTGAATTCC CGTCCTCAA ATAATGTTAC
3275 3280 3285 3290 3295 3300 3305 3310 3315 3320 3325 3330
* * * * * * * * * * * *
TATCTTTATT AAAACAAAAG GGTGTATAGT GTTCACAAAC TGTGAAAATA GTGTAAGAAC
ATAGAAATAA TTTTGTTC CCACATATCA CAAGTGTGTTG ACACTTTAT CACATTCTTG
3335 3340 3345 3350 3355 3360 3365 3370 3375 3380 3385 3390
* * * * * * * * * * * *
TGTACATTGT GAGCTCTGGT TATTTTCTC TTGTACCATA GAAAAATGTA TAAAAATTAT
ACATGTAACA CTCGAGACCA ATAAAAAGAG AACATGGTAT CTTTTTACAT ATTTTTAATA
3395 3400 3405 3410 3415 3420 3425 3430 3435 3440 3445 3450
* * * * * * * * * * * *
CAAAAAGCTA ATGTGCAGGG ATATTGCCCTT ATTTGTCTGT AAAAAATGGA GCTCAGTAAC
GTTTTTCGAT TACACGTCCC TATAACGGAA TAAACAGACA TTTTTTACCT CGAGTCATTG
3455 3460 3465 3470 3475 3480 3485 3490 3495
* * * * * * * * * * * *
ATAACTGCTT CTTGGAGCTT TGGAATATTT TATCCTGTAT TCTTGTGTT (SEQ ID NO:5)
TATTGACGAA GAACCTCGAA ACCTTATAAA ATAGGACATA AGAACAAA

FIG. 7

5 10 15 20 25 30 35 40 45 50
 CAACA ATG GCG GCT CCG AGC CCG AGC GGT GGC GGC GGC AGC GGC ACC CCC
 GTTGT TAC CGC CGA GGC TCG GGC TCG CCA CCG CCG TCG CCG TGG GGG
 Met Ala Ala Pro Ser Pro Ser Gly Gly Gly Ser Gly Thr Pro>

 55 60 65 70 75 80 85 90 95
 GGC CCC GTA GGG TCC CCG GCG CCA GGC CAC CCG GCC GTC AGC AGC ATG
 CCG GGG CAT CCC AGG GGC CGC GGT CCG GTG GGC CGG CAG TCG TCG TAC
 Gly Pro Val Gly Ser Pro Ala Pro Gly His Pro Ala Val Ser Ser Met>

 100 105 110 115 120 125 130 135 140 145
 * * * * * * * * *
 CAG GGT AAA CGC AAA GCA CTG AAG TTG AAT TTT GCA AAT CCA CCT TTC
 GTC CCA TTT GCG TTT CGT GAC TTC AAC TTA AAA CGT TTA GGT GGA AAG
 Gln Gly Lys Arg Lys Ala Leu Lys Leu Asn Phe Ala Asn Pro Pro Phe>

 150 155 160 165 170 175 180 185 190
 * * * * * * * *
 AAA TCT ACA GCA AGG TTT ACT CTG AAT CCC AAT CCT ACA GGA GTT CAA
 TTT AGA TGT CGT TCC AAA TGA GAC TTA GGG TTA GGA TGT CCT CAA GTT
 Lys Ser Thr Ala Arg Phe Thr Leu Asn Pro Asn Pro Thr Gly Val Gln>

 195 200 205 210 215 220 225 230 235 240
 * * * * * * * * *
 AAC CCA CAC ATA GAG AGA CTG AGA ACA CAC AGC ATT GAG TCA TCA GGA
 TTG GGT GTG TAT CTC TCT GAC TCT TGT GTG TCG TAA CTC AGT AGT CCT
 Asn Pro His Ile Glu Arg Leu Arg Thr His Ser Ile Glu Ser Ser Gly>

 245 250 255 260 265 270 275 280 285 290
 * * * * * * * * *
 AAA CTG AAG ATC TCC CCT GAA CAA CAC TGG GAT TTC ACT GCA GAG GAC
 TTT GAC TTC TAG AGG GGA CTT GTT GTG ACC CTA AAG TGA CGT CTC CTG
 Lys Leu Lys Ile Ser Pro Glu Gln His Trp Asp Phe Thr Ala Glu Asp>

 295 300 305 310 315 320 325 330 335
 * * * * * * * *
 TTG AAA GAC CTT GGA GAA ATT GGA CGA GGA GCT TAT GGT TCT GTC AAC
 AAC TTT CTG GAA CCT CTT TAA CCT GCT CCT CGA ATA CCA AGA CAG TTG
 Leu Lys Asp Leu Gly Ile Gly Arg Gly Ala Tyr Gly Ser Val Asn>

 340 345 350 355 360 365 370 375 380 385
 * * * * * * * * *
 AAA ATG GTC CAC AAA CCA AGT GGG CAA ATA ATG GCA GTT AAA AGA ATT
 TTT TAC CAG GTG TTT GGT TCA CCC GTT TAT TAC CGT CAA TTT TCT TAA
 Lys Met Val His Lys Pro Ser Gly Gln Ile Met Ala Val Lys Arg Ile>

 390 395 400 405 410 415 420 425 430
 * * * * * * * *
 CGG TCA ACA GTG GAT GAA AAA GAA CAA AAA CAA CTT CTT ATG GAT TTG
 GCC AGT TGT CAC CTA CTT TTT CTT GTT TTT GTT GAA GAA TAC CTA AAC
 Arg Ser Thr Val Asp Glu Lys Glu Gln Lys Gln Leu Leu Met Asp Leu>

 435 440 445 450 455 460 465 470 475 480
 * * * * * * * *
 GAT GTA GTA ATG CGG AGT AGT GAT TGC CCA TAC ATT GTT CAG TTT TAT
 CTA CAT CAT TAC GCC TCA TCA CTA ACG GGT ATG TAA CAA GTC AAA ATA
 Asp Val Val Met Arg Ser Ser Asp Cys Pro Tyr Ile Val Gln Phe Tyr>

FIG. 7 - CONT'D

485 490 495 500 * 505 510 515 520 525 530
 * * * * * * * * * *
 GGT GCA CTC TTC AGA GAG GGT GAC TGT TGG ATC TGT ATG GAA CTC ATG
 CCA CGT GAG AAG TCT CTC CCA CTG ACA ACC TAG ACA TAC CTT GAG TAC
 Gly Ala Leu Phe Arg Glu Gly Asp Cys Trp Ile Cys Met Glu Leu Met>

 535 540 545 550 * 555 560 * 565 570 575
 * * * * * * * * * *
 TCT ACC TCG TTT GAT AAG TTT TAC AAA TAT GTA TAT AGT GTA TTA GAT
 AGA TGG AGC AAA CTA TTC AAA ATG TTT ATA CAT ATA TCA CAT AAT CTA
 Ser Thr Ser Phe Asp Lys Phe Tyr Lys Tyr Val Tyr Ser Val Leu Asp>

 580 585 590 595 600 * 605 610 * 615 620 625
 * * * * * * * * * *
 GAT GTT ATT CCA GAA GAA ATT TTA GGC AAA ATC ACT TTA GCA ACT GTG
 CTA CAA TAA GGT CTT CTT TAA AAT CCG TTT TAG TGA AAT CGT TGA CAC
 Asp Val Ile Pro Glu Glu Ile Leu Gly Lys Ile Thr Leu Ala Thr Val>

 630 635 640 645 650 * 655 660 * 665 670
 * * * * * * * * * *
 AAA GCA CTA AAC CAC TTA AAA GAA AAC TTG AAA ATT ATT CAC AGA GAT
 TTT CGT GAT TTG GTG AAT TTT CTT TTG AAC TTT TAA TAA GTG TCT CTA
 Lys Ala Leu Asn His Leu Lys Glu Asn Leu Lys Ile Ile His Arg Asp>

 675 680 685 690 * 695 700 * 705 710 715 720
 * * * * * * * * * *
 ATC AAA CCT TCC AAT ATT CTT CTG GAC AGA AGT GGA AAT ATT AAG CTC
 TAG TTT GGA AGG TTA TAA GAA GAC CTG TCT TCA CCT TTA TAA TTC GAG
 Ile Lys Pro Ser Asn Ile Leu Leu Asp Arg Ser Gly Asn Ile Lys Leu>

 725 730 735 740 * 745 750 * 755 760 765 770
 * * * * * * * * * *
 TGT GAC TTC GGC ATC AGT GGA CAG CTT GTG GAC TCT ATT GCC AAG ACA
 ACA CTG AAG CCG TAG TCA CCT GTC GAA CAC CTG AGA TAA CGG TTC TGT
 Cys Asp Phe Gly Ile Ser Gly Gln Leu Val Asp Ser Ile Ala Lys Thr>

 775 780 785 790 * 795 800 * 805 810 815
 * * * * * * * * * *
 AGA GAT GCT GGC TGT AGG CCA TAC ATG GCA CCT GAA AGA ATA GAC CCA
 TCT CTA CGA CCG ACA TCC GGT ATG TAC CGT GGA CTT TCT TAT CTG GGT
 Arg Asp Ala Gly Cys Arg Pro Tyr Met Ala Pro Glu Arg Ile Asp Pro>

 820 825 830 * 835 840 * 845 850 * 855 860 865
 * * * * * * * * * *
 AGC GCA TCA CGA CAA GGA TAT GAT GTC CGC TCT GAT GTC TGG AGT TTG
 TCG CGT AGT GCT GTT CCT ATA CTA CAG GCG AGA CTA CAG ACC TCA AAC
 Ser Ala Ser Arg Gln Gly Tyr Asp Val Arg Ser Asp Val Trp Ser Leu>

 870 875 880 885 890 * 895 900 * 905 910
 * * * * * * * * * *
 GGG ATC ACA TTG TAT GAG TTG GCC ACA GGC CGA TTT CCT TAT CCA AAG
 CCC TAG TGT AAC ATA CTC AAC CGG TGT CCG GCT AAA GGA ATA GGT TTC
 Gly Ile Thr Leu Tyr Glu Leu Ala Thr Gly Arg Phe Pro Tyr Pro Lys>

 915 920 925 930 * 935 940 * 945 950 * 955 960
 * * * * * * * * * *
 TGG AAT AGT GTA TTT GAT CAA CTA ACA CAA GTC GTG AAA GGA GAT CCT
 ACC TTA TCA CAT AAA CTA GTT GAT TGT GTT CAG CAC TTT CCT CTA GGA
 Trp Asn Ser Val Phe Asp Gln Leu Thr Gln Val Val Lys Gly Asp Pro>

 965 970 975 980 * 985 990 * 995 1000 * 1005 1010
 * * * * * * * * * *

FIG. 7 - CONT'D

CGG CAG CTG AGT AAT TCT GAG GAA AGG GAA TTC TCC CCG AGT TTC ATC
 GGC GTC GAC TCA TTA AGA CTC CTT TCC CTT AAG AGG GGC TCA AAG TAG
 Pro Gln Leu Ser Asn Ser Glu Glu Arg Glu Phe Ser Pro Ser Phe Ile>

 1015 1020 1025 1030 1035 1040 1045 1050 1055
 * * * * * * * * *
 AAC TTT GTC AAC TTG TGC CTT ACG AAG GAT GAA TCC AAA AGG CCA AAG
 TTG AAA CAG TTG AAC ACG GAA TGC TTC CTA CTT AGG TTT TCC GGT TTC
 Asn Phe Val Asn Leu Cys Leu Thr Lys Asp Glu Ser Lys Arg Pro Lys>

 1060 1065 1070 1075 1080 1085 1090 1095 1100 1105
 * * * * * * * * *
 TAT AAA GAG CTT CTG AAA CAT CCC TTT ATT TTG ATG TAT GAA GAA CGT
 ATA TTT CTC GAA GAC TTT GTA GGG AAA TAA AAC TAC ATA CTT CTT GCA
 Tyr Lys Glu Leu Leu Lys His Pro Phe Ile Leu Met Tyr Glu Glu Arg>

 1110 1115 1120 1125 1130 1135 1140 1145 1150
 * * * * * * * * *
 GCC GTT GAG GTC GCA TGC TAT GTT TGT AAA ATC CTG GAT CAA ATG CCA
 CGG CAA CTC CAG CGT ACG ATA CAA ACA TTT TAG GAC CTA GTT TAC GGT
 Ala Val Glu Val Ala Cys Tyr Val Cys Lys Ile Leu Asp Gln Met Pro>

 1155 1160 1165 1170 1175 1180 1185 1190 1195 1200
 * * * * * * * * *
 GCT ACT CCC AGC TCT CCC ATG TAT GTC GAT TGATAT CGYTGCTACA
 CGA TGA GGG TCG AGA GGG TAC ATA CAG CTA ACTATA GCRACGATGT
 Ala Thr Pro Ser Ser Pro Met Tyr Val Asp> (SEQ ID NO:8)

 1205 1210 1215 1220 1225 1230 1235 1240 1245 1250 1255 1260
 * * * * * * * * *
 TCAGACTCTA GAAAAAAGGG CTGAGAGGAA GCAAGACGTA AAGAATTTC ATCCCGTATC
 AGTCTGAGAT CTTTTTCCC GACTCTCCTT CGTTCTGCAT TTCTTAAAG TAGGGCATAG

 1265 1270 1275 1280 1285 1290 1295 1300 1305 1310 1315 1320
 * * * * * * * * *
 ACAGTGTTTT TATTGCTCGC CCAGACACCA TGTGCAATAA GATTGGTGT CGTTTCCATC
 TGTACAAAA ATAACGAGCG GGTCTGTGGT ACACGTTATT CTAACCACAA GCAAAGGTAG

 1325 1330 1335 1340 1345 1350 1355 1360 1365 1370 1375 1380
 * * * * * * * * *
 ATGTCCTGTAT ACTCCTGTCA CCTAGAACGT GCATCCTGT AATAACCTGAT TGATCACACA
 TACAGACATA TGAGGACAGT GGATCTTGCA CGTAGGAACA TTATGGACTA ACTAGTGTGT

 1385 1390 1395 1400 1405 1410 1415 1420 1425 1430 1435 1440
 * * * * * * * * *
 GTGTTAGTGC TGGTCAGAGA GACCTCATCC TGCTCTTTTG TGATGAACAT ATTCAATGAAA
 CACAATCACG ACCAGTCTCT CTGGAGTAGG ACAGAGAAAAC ACTACTGTAA TAAGTACTTT

 1445 1450 1455 1460 1465 1470 1475 1480 1485 1490 1495 1500
 * * * * * * * * *
 TGTGGAAGTC AGTACGATCA AGTTGTTGAC TGTGATTAGA TCACATCTTA AATTCAATTTC
 ACACCTTCAG TCATGCTAGT TCAACAACTG ACACAAATCT AGTGTAGAAT TTAAGTAAAG

 1505 1510 1515 1520 1525 1530 1535 1540 1545 1550 1555 1560
 * * * * * * * * *
 TAGACTCAAAC ACCTGGAGAT GCAGCTACTG GAATGGTGT TTGTCAGACT TCCAAATCCT
 ATCTGAGTTT TGGACCTCTA CGTCGATGAC CTTACCACAA AACAGTCTGA AGGTTTAGGA

 1565 1570 1575 1580 1585 1590 1595 1600 1605 1610 1615 1620
 * * * * * * * * *
 GGAAGGACAC AGTGATGAAT GTACTATATC TGAACATAGA AAACTCGGGCT TGAGTGAGAA
 CCTTCCTGTG TCACTACTTA CATGATATAG ACTTGTATCT TTGAGCCCCGA ACTCACTCTT

FIG. 7 - CONT'D

1625 1630 1635 1640 1645 1650 1655 1660 1665 1670 1675 1680
 * * * * * * * * * * * *
 GAGCTTGCAC AGCCAACGAG ACACATTGCC TTCTGGAGCT GGGAGACAAA GGAGGAATTT
 CTCGAACGTG TCGGTTCGTC TGTGTAACGG AAGACCTCGA CCCTCTGTTT CCTCCTTAAA

 1685 1690 1695 1700 1705 1710 1715 1720 1725 1730 1735 1740
 * * * * * * * * * * * *
 ACTTTCTTCA CCAAGTGCAA TAGATTACTG ATGTGATATT CTGTTGCTTT ACAGTTACAG
 TGAAAGAAGT GGTTCACGTT ATCTAATGAC TACACTATAA GACAACGAAA TGTCAATGTC

 1745 1750 1755 1760 1765 1770 1775 1780 1785 1790 1795 1800
 * * * * * * * * * * * *
 TTGATGTTTG GGGATCGATG TGCTCAGCCA AATTCCTGT TTGAAATATC ATGTTAAATT
 AACTACAAAC CCCTAGCTAC ACGAGTCGGT TTAAAGGACA AACTTTATAG TACAATTAA

 1805 1810 1815 1820 1825 1830 1835 1840 1845 1850 1855 1860
 * * * * * * * * * * * *
 AGAACATGAATT TATCTTTACC AAAAACCATG TTGCGTTCAA AGAGGTGAAC ATTAAAATAT
 TCTTACTTAA ATAGAAATGG TTTTGGTAC AACGCAAGTT TCTCCACTTG TAATTAA

 1865 1870 1875 1880 1885 1890 1895 1900 1905 1910 1915 1920
 * * * * * * * * * * * *
 AGAGACAGGA CAGAATGTGT TCTTTCTCC TCTACCAGTC CTATTTTCA ATGGGAAGAC
 TCTCTGTCCT GTCTTACACA AGAAAAGAGG AGATGGTCAG GATAAAAAGT TACCCTTCTG

 1925 1930 1935 1940 1945 1950 1955 1960 1965 1970 1975 1980
 * * * * * * * * * * * *
 TCAGGAGTCT GCCACTTGTG AAAGAAGGTG CTGATCCTAA GAATTTTCA TTCTCAGAAT
 AGTCCTCAGA CGGTGAACAG TTTCTCCAC GACTAGGATT CTTAAAAAGT AAGAGTCTTA

 1985 1990 1995 2000 2005 2010 2015 2020 2025 2030 2035 2040
 * * * * * * * * * * * *
 TCGGTGTGCT GCCAACTTGA TGTTCCACCT GCCACAAACC ACCAGGACTG AAAGAAGAAA
 AGCCACACGA CGGTTGAACG ACAAGGTGGA CGGTGTTGG TGGCCTGAC TTTCTTCTT

 2045 2050 2055 2060 2065 2070 2075 2080 2085 2090 2095 2100
 * * * * * * * * * * * *
 ACAGTACAGA AGGCAAAGTT TACAGATGTG TTTAATTCTA GTATTTTATC TGGAAACAAT
 TGTCACTGTCT TCCGTTTCAA ATGTCTACAA AAATTAAGAT CATAAAATAG ACCTTGTGTA

 2105 2110 2115 2120 2125 2130 2135 2140 2145 2150 2155 2160
 * * * * * * * * * * * *
 TGTAGCAGCT ATATATTICC CCTTGGTCCC AAGCCTGATA CTTTAGCCAT CATAACTCAC
 ACATCGTCGA TATATAAAGG GGAACCAGGG TTCGGACTAT GAAATCGGT A TATTGAGTG

 2165 2170 2175 2180 2185 2190 2195 2200 2205 2210 2215 2220
 * * * * * * * * * * * *
 TAACAGGGAG AAGTAGCTAG TAGCAATGTG CCTTGATTGA TTAGATAAAG ATTTCTAGTA
 ATTGTCCCTC TTCATCGATC ATCGTTACAC GGAACACTA AATCTATTTC TAAAGATCAT

 2225 2230 2235 2240 2245 2250 2255 2260 2265 2270 2275 2280
 * * * * * * * * * * * *
 GGCAGCAAAA GACCAAATCT CAGTTGTTTG CCTCTTGCCA TCACTGGTCC AGGTCTTCAG
 CCGTCGTTT CTGGTTAGA GTCAACAAAC GAAGAACGGT AGTGACCAGG TCCAGAAGTC

 2285 2290 2295 2300 2305 2310 2315 2320 2325 2330 2335 2340
 * * * * * * * * * * * *
 TTTCGAATC TCTTTCCCTT CCCCTGTGGT CTATTGTCGC TATGTGACTT CGGCCTAAATC
 AAAGGCTTAG AGAAAGGGAA GGGGACACCA GATAACAGCG ATACACTGAA CGCGAATTAG

 2345 2350 2355 2360 2365 2370 2375 2380 2385 2390 2395 2400

FIG. 7 - CONT'D

CAATATTTTG CCTTTTTCT ATATCAAAAA ACCTTTACAG TTAGCAGGGA TGTCCTTAC
 GTTATAAAAC GGAAAAAAGA TATAGTTTT TGAAATGTC AATCGTCCCT ACAAGGAATG
 2405 2410 2415 2420 2425 2430 2435 2440 2445 2450 2455 2460
 * * * * * * * * * * * *
 CGAGGATTT TAACCCCCAA TCTCTCATAA TCGCTAGTGT TTAAAAGGCT AAGAATAGTG
 GCTCCTAAAA ATTGGGGTT AGAGAGTATT AGCGATCACA AATTTCCGA TTCTTATCAC
 2465 2470 2475 2480 2485 2490 2495 2500 2505 2510 2515 2520
 * * * * * * * * * * * *
 GGGCCAACC GATGTGGTAG GTGATAAAGA GGCATCTTT CTAGAGACAC ATTGGACCAG
 CCCGGGTTGG CTACACCAC CACTATTCT CGTAGAGAAA GATCTCTGTG TAACCTGGTC
 2525 2530 2535 2540 2545 2550 2555 2560 2565 2570 2575 2580
 * * * * * * * * * * * *
 ATGAGGATCC GAAACGGCAG CCTTACGTT CATCACCTGC TAGAACCTCT CGTAGTCCAT
 TACTCCTAGG CTTGCCGTC GGAAATGCAA GTAGTGGACG ATCTTGGAGA GCATCAGGTA
 2585 2590 2595 2600 2605 2610 2615 2620 2625 2630 2635 2640
 * * * * * * * * * * * *
 CACCATTTCT TGGCATTGGA ATTCTACTGG AAAAAAAATAC AAAAAGCAA ACAAAACCCCT
 GTGGTAAAGA ACCGTAACCT TAAGATGACC TTTTTTATG TTTTCGTTT TGTTTGGGA
 2645 2650 2655 2660 2665 2670 2675 2680 2685 2690 2695 2700
 * * * * * * * * * * * *
 CAGCACTGTT ACAAGAGGCC ATTTAAGTAT CTTGTGCTTC TTCACTTACC CATTAGCCAG
 GTCGTGACAA TGTCTCCTGG TAAATTCTAA GAACACGAAG AAGTGAATGG GTAATCGGTC
 2705 2710 2715 2720 2725 2730 2735 2740 2745 2750 2755 2760
 * * * * * * * * * * * *
 GTTCTCATTA GGTTTGCTT GGGCCTCCCT GGCACTGAAC CTTAGGCTTT GTATGACAGT
 CAAGAGTAAT CCAAACGAA CCCGGAGGGA CGTGACTTG GAATCCGAAA CATACTGTCA
 2765 2770 2775 2780 2785 2790 2795 2800 2805 2810 2815 2820
 * * * * * * * * * * * *
 GAAGCAGCAC TGTGAGTGGT TCAAGCACAC TGGAATATAA AACAGTCATG GCCTGAGATG
 CTTCGTCGTG ACACTCACCA AGTTCGTGTG ACCTTATATT TTGTCAGTAC CGGACTCTAC
 2825 2830 2835 2840 2845 2850 2855 2860 2865 2870 2875 2880
 * * * * * * * * * * * *
 CAGGTGATGC CATTACAGAA CCAAATCGTG GCACGTATTG CTGTGTCCTC TCTCAGAGTG
 GTCCACTACG GTAAATGTCTT GGTTAGCAC CGTGCATAAC GACACAGAGG AGAGTCTCAC
 2885 2890 2895 2900 2905 2910 2915 2920 2925 2930 2935 2940
 * * * * * * * * * * * *
 ACAGTCATAA ATACTGTCAA ACAATAAAGG GAGAATGGTG CTGTTTAAAG TCACATCCCT
 TGTCAGTATT TATGACAGTT TGTATTTCCT CTCTTACAC GACAAATTTC AGTGTAGGGA
 2945 2950 2955 2960 2965 2970 2975 2980 2985 2990 2995 3000
 * * * * * * * * * * * *
 GTAAATTGCA GAATTCAAAA GTGATTATCT CTTTGATCTA CTTGCCTCAT TTCCCTATCT
 CATTAAACGT CTTAAGTTTT CACTAATAGA GAAACTAGAT GAACGGAGTA AAGGGATAGA
 3005 3010 3015 3020 3025 3030 3035 3040 3045 3050 3055 3060
 * * * * * * * * * * * *
 TCTCCCCCAC GGTATCCTAA ACTTTAGACT TCCCACGTGT CTGAAAGGAG ACATTGCTCT
 AGAGGGGGTG CCATAGGATT TGAAATCTGA AGGGTGACAA GACTTTCCCT TGTAACGAGA
 3065 3070 3075 3080 3085 3090 3095 3100 3105 3110 3115 3120
 * * * * * * * * * * * *

ATGTCTGCCT TCGACCACAG CAAGCCATCA TCCTCCATTG CTCCCGGGGA CTCAAGAGGA

FIG. 7 - CONT'D

TA~~C~~AGACGGA AGCTGGTGTC GTTCGGTAGT AGGAGGTAAC GAGGGCCCCT GAGTTCTCCT
3125 3130 3135 3140 3145 3150 3155 3160 3165 3170 3175 3180
* * * * * * * * * * * *
ATCTGTTCT CTGCTGTCAA CTTCCCATCT GGCTCAGCAT AGGGTCACTT TGCCATTATG
TAGACAAAGA GACGACAGTT GAAGGGTAGA CCGAGTCGTA TCCCACTGAA ACGGTAATAC
3185 3190 3195 3200 3205 3210 3215 3220 3225 3230 3235 3240
* * * * * * * * * * * *
CAAATGGAGA TAAAAGCAAT TCTGGCTGTC CAGGAGCTAA TCTGACCGTT CTATTGTGTG
GTTTACCTCT ATTTTCGTAA AGACCGACAG GTCCTCGATT AGACTGGCAA GATAACACAC
3245 3250 3255 3260 3265 3270 3275 3280 3285 3290 3295 3300
* * * * * * * * * * * *
GATGACCACA TAAGAAGGCA ATTTTAGTGT ATTAATCATA GATTATTATA AACTATAAAC
CTACTGGTGT ATTCTTCCGT TAAAATCACA TAATTAGTAT CTAATAATAT TTGATATTG
3305 3310 3315 3320 3325 3330 3335 3340 3345 3350 3355 3360
* * * * * * * * * * * *
TTAAGGGCAA GGAGTTTATT ACAATGTATC TTTATTAAAA CAAAAGGGTG TATAGTGTTC
AATTCCCGTT CCTCAAATAA TGTTACATAG AAATAATTIT GTTTCCCAC ATATCACAAG
3365 3370 3375 3380 3385 3390 3395 3400 3405 3410 3415 3420
* * * * * * * * * * * *
ACAAACTGTG AAAATAGTGT AAGAACTGTA CATTGTGAGC TCTGGTTATT TTTCTCTTGT
TGTTTGACAC TTTTATCACA TTCTTGACAT GTAACACTCG AGACCAATAA AAAGAGAAACA
3425 3430 3435 3440 3445 3450 3455 3460 3465 3470 3475 3480
* * * * * * * * * * * *
ACCATAGAAA AATGTATAAA AATTATCAAA AAGCTAATGT GCAGGGATAT TGCCCTTATTT
TGGTATCTTT TTACATATTT TTAATAGTTT TTCGATTACA CGTCCCTATA ACGGAATAAA
3485 3490 3495 3500 3505 3510 3515 3520 3525 3530 3535 3540
* * * * * * * * * * * *
GTCTGTAAAA AATGGAGCTC AGTAACATAA CTGCTTCTTG GAGCTTTGGA ATATTTATC
CAGACATTTT TTACCTCGAG TCATTGTATT GACGAAGAAC CTCGAAACCT TATAAAATAG
3545 3550
*
CTGTATTCCTT GTTT (SEQ ID NO:7)
GACATAAGAA CAAA

FIG. 8

5	10	15	20	25	30	35	40	45	50
*	*	*	*	*	*	*	*	*	*
CTCCCAACA ATG GCG GCT CCG AGC CCG AGC GGC GGC GGC GGC TCC GGG GGC GAGGGTTGT TAC CGC CGA GGC TCG GGC TCG CCG CCG CCC AGG CCC CCG Met Ala Ala Pro Ser Pro Ser Gly Gly Gly Ser Gly Gly >									
55	60	65	70	75	80	85	90	95	
*	*	*	*	*	*	*	*	*	
GGC AGC GGC AGC GGC ACC CCC GGC CCC GTA GGG TCC CCG GCG CCA GGC CCG TCG CCG TCG CCG TGG GGG CCG GGG CAT CCC AGG GGC CGC GGT CCG Gly Ser Gly Ser Gly Thr Pro Gly Pro Val Gly Ser Pro Ala Pro Gly >									
100	105	110	115	120	125	130	135	140	145
*	*	*	*	*	*	*	*	*	
CAC CCG GCC GTC AGC AGC ATG CAG GGT AAA CGC AAA GCA CTG AAG TTG GTG GGC CGG CAG TCG TCG TAC GTC CCA TTT GCG TTT CGT GAC TTC AAC His Pro Ala Val Ser Ser Met Gln Gly Lys Arg Lys Ala Leu Lys Leu >									
150	155	160	165	170	175	180	185	190	195
*	*	*	*	*	*	*	*	*	
AAT TTT GCA AAT CCA CCT TTC AAA TCT ACA GCA AGG TTT ACT CTG AAT TTA AAA CGT TTA GGT GGA AAG TTT AGA TGT CGT TCC AAA TGA GAC TTA Asn Phe Ala Asn Pro Pro Phe Lys Ser Thr Ala Arg Phe Thr Leu Asn >									
200	205	210	215	220	225	230	235	240	
*	*	*	*	*	*	*	*	*	
CCC AAT CCT ACA GGA GTT CAA AAC CCA CAC ATA GAG AGA CTG AGA ACA GGG TTA GGA TGT CCT CAA GTT TTG GGT GTG TAT CTC TCT GAC TCT TGT Pro Asn Pro Thr Gly Val Gln Asn Pro His Ile Glu Arg Leu Arg Thr >									
245	250	255	260	265	270	275	280	285	290
*	*	*	*	*	*	*	*	*	
CAC AGC ATT GAG TCA TCA GGA AAA CTG AAG ATC TCC CCT GAA CAA CAC GTG TCG TAA CTC AGT AGT CCT TTT GAC TTC TAG AGG GGA CTT GTT GTG His Ser Ile Glu Ser Ser Gly Lys Leu Lys Ile Ser Pro Glu Gln His >									
295	300	305	310	315	320	325	330	335	
*	*	*	*	*	*	*	*	*	
TGG GAT TTC ACT GCA GAG GAC TTG AAA GAC CTT GGA GAA ATT GGA CGA ACC CTA AAG TGA CGT CTC CTG AAC TTT CTG GAA CCT CTT TAA CCT GCT Trp Asp Phe Thr Ala Glu Asp Leu Lys Asp Leu Gly Glu Ile Gly Arg >									
340	345	350	355	360	365	370	375	380	385
*	*	*	*	*	*	*	*	*	
GGA GCT TAT GGT TCT GTC AAC AAA ATG GTC CAC AAA CCA AGT GGG CAA CCT CGA ATA CCA AGA CAG TTG TTT TAC CAG GTG TTT GGT TCA CCC GTT Gly Ala Tyr Gly Ser Val Asn Lys Met Val His Lys Pro Ser Gly Gln >									
390	395	400	405	410	415	420	425	430	435
*	*	*	*	*	*	*	*	*	
ATA ATG GCA GTT AAA AGA ATT CGG TCA ACA GTG GAT GAA AAA GAA CAA TAT TAC CGT CAA TTT TCT TAA GCC AGT TGT CAC CTA CTT TTT CTT GTT Ile Met Ala Val Lys Arg Ile Arg Ser Thr Val Asp Glu Lys Glu Gln >									
440	445	450	455	460	465	470	475	480	
*	*	*	*	*	*	*	*	*	
AAA CAA CTT CTT ATG GAT TTG GAT GTA GTA ATG CGG AGT AGT GAT TGC TTT GTT GAA GAA TAC CTA AAC CTA CAT CAT TAC GCC TCA TCA CTA ACG Lys Gln Leu Leu Met Asp Leu Asp Val Val Met Arg Ser Ser Asp Cys >									

FIG. 8 - CONT'D

485 490 495 500 505 510 515 520 525 530
 * * * * * * * * * *
 CCA TAC ATT GTT CAG TTT TAT GGT GCA CTC TTC AGA GAG GGT GAC TGT
 GGT ATG TAA CAA GTC AAA ATA CCA CGT GAG AAG TCT CTC CCA CTG ACA
 Pro Tyr Ile Val Gln Phe Tyr Gly Ala Leu Phe Arg Glu Gly Asp Cys>

 535 540 545 550 555 560 565 570 575
 * * * * * * * * *
 TGG ATC TGT ATG GAA CTC ATG TCT ACC TCG TTT GAT AAG TTT TAC AAA
 ACC TAG ACA TAC CTT GAG TAC AGA TGG AGC AAA CTA TTC AAA ATG TTT
 Trp Ile Cys Met Glu Leu Met Ser Thr Ser Phe Asp Lys Phe Tyr Lys>

 580 585 590 595 600 605 610 615 620 625
 * * * * * * * * * *
 TAT GTA TAT AGT GTA TTA GAT GAT GTT ATT CCA GAA GAA ATT TTA GGC
 ATA CAT ATA TCA CAT AAT CTA CTA CAA TAA GGT CTT CTT TAA AAT CCG
 Tyr Val Tyr Ser Val Leu Asp Asp Val Ile Pro Glu Ile Leu Gly>

 630 635 640 645 650 655 660 665 670 675
 * * * * * * * * * *
 AAA ATC ACT TTA GCA ACT GTG AAA GCA CTA AAC CAC TTA AAA GAA AAC
 TTT TAG TGA AAT CGT TGA CAC TTT CGT GAT TTG GTG AAT TTT CTT TTG
 Lys Ile Thr Leu Ala Thr Val Lys Ala Leu Asn His Leu Lys Glu Asn>

 680 685 690 695 700 705 710 715 720
 * * * * * * * * * *
 TTG AAA ATT ATT CAC AGA GAT ATC AAA CCT TCC AAT ATT CTT CTG GAC
 AAC TTT TAA TAA GTG TCT CTA TAG TTT GGA AGG TTA TAA GAA GAC CTG
 Leu Lys Ile Ile His Arg Asp Ile Lys Pro Ser Asn Ile Leu Leu Asp>

 725 730 735 740 745 750 755 760 765 770
 * * * * * * * * * *
 AGA AGT GGA AAT ATT AAG CTC TGT GAC TTC GGC ATC AGT GGA CAG CTT
 TCT TCA CCT TTA TAA TTC GAG ACA CTG AAG CCG TAG TCA CCT GTC GAA
 Arg Ser Gly Asn Ile Lys Leu Cys Asp Phe Gly Ile Ser Gly Gln Leu>

 775 780 785 790 795 800 805 810 815
 * * * * * * * * * *
 GTG GAC TCT ATT GCC AAG ACA AGA GAT GCT GGC TGT AGG CCA TAC ATG
 CAC CTG AGA TAA CGG TTC TGT TCT CTA CGA CCG ACA TCC GGT ATG TAC
 Val Asp Ser Ile Ala Lys Thr Arg Asp Ala Gly Cys Arg Pro Tyr Met>

 820 825 830 835 840 845 850 855 860 865
 * * * * * * * * * *
 GCA CCT GAA AGA ATA GAC CCA AGC GCA TCA CGA CAA GGA TAT GAT GTC
 CGT GGA CTT TCT TAT CTG GGT TCG CGT AGT GCT GTT CCT ATA CTA CAG
 Ala Pro Glu Arg Ile Asp Pro Ser Ala Ser Arg Gln Gly Tyr Asp Val>

 870 875 880 885 890 895 900 905 910 915
 * * * * * * * * * *
 CGC TCT GAT GTC TGG AGT TTG GGG ATC ACA TTG TAT GAG TTG GCC ACA
 GCG AGA CTA CAG ACC TCA AAC CCC TAG TGT AAC ATA CTC AAC CGG TGT
 Arg Ser Asp Val Trp Ser Leu Gly Ile Thr Leu Tyr Glu Leu Ala Thr>

 920 925 930 935 940 945 950 955 960
 * * * * * * * * * *
 GGC CGA TTT CCT TAT CCA AAG TGG AAT AGT GTA TTT GAT CAA CTA ACA
 CCG GCT AAA GGA ATA GGT TTC ACC TTA TCA CAT AAA CTA GTT GAT TGT
 Gly Arg Phe Pro Tyr Pro Lys Trp Asn Ser Val Phe Asp Gln Leu Thr>

 965 970 975 980 985 990 995 1000 1005 1010
 * * * * * * * * * *

FIG. 8 - CONT'D

CAA GTC GTG AAA GGA GAT CCT CCG CAG CTG AGT AAT TCT GAG GAA AGG
 GTT CAG CAC TTT CCT CTA GGA GGC GTC GAC TCA TTA AGA CTC CTT TCC
 Gln Val Val Lys Gly Asp Pro Pro Gln Leu Ser Asn Ser Glu Glu Arg>

1015 1020 1025 1030 1035 1040 1045 1050 1055

*
 GAA TTC TCC CCG AGT TTC ATC AAC TTT GTC AAC TTG TGC CTT ACG AAG
 CTT AAG AGG GGC TCA AAG TAG TTG AAA CAG TTG AAC ACG GAA TGC TTC
 Glu Phe Ser Pro Ser Phe Ile Asn Phe Val Asn Leu Cys Leu Thr Lys>

1060 1065 1070 1075 1080 1085 1090 1095 1100 1105

*
 *
 GAT GAA TCC AAA AGG CCA AAG TAT AAA GAG CTT CTG AAA CAT CCC TTT
 CTA CTT AGG TTT TCC GGT TTC ATA TTT CTC GAA GAC TTT GTA GGG AAA
 Asp Glu Ser Lys Arg Pro Lys Tyr Lys Glu Leu Leu Lys His Pro Phe>

1110 1115 1120 1125 1130 1135 1140 1145 1150 1155

*
 ATT TTG ATG TAT GAA GAA CGT GCC GTT GAG GTC GCA TGC TAT GTT TGT
 TAA AAC TAC ATA CTT CTT GCA CGG CAA CTC CAG CGT ACG ATA CAA ACA
 Ile Leu Met Tyr Glu Glu Arg Ala Val Glu Val Ala Cys Tyr Val Cys>

1160 1165 1170 1175 1180 1185 1190 1195 1200

*
 *
 AAA ATC CTG GAT CAA ATG CCA GCT ACT CCC AGC TCT CCC ATG TAT GTC
 TTT TAG GAC CTA GTT TAC GGT CGA TGA GGG TCG AGA GGG TAC ATA CAG
 Lys Ile Leu Asp Gln Met Pro Ala Thr Pro Ser Ser Pro Met Tyr Val>

1205 1210 1215 1220 1225 1230 1235 1240 1245 1250 1255 1260

*
 *
 GAT TGAT ATCGCTGCTA CATCAGACTC TAGAAAAAAG GGCTGAGAGG AAGCAAGACG
 CTA ACTA TAGCGACGAT GTAGTCTGAG ATCTTTTTTC CCGACTCTCC TTCGTTCTGC
 Asp> (SEQ ID NO:10)

1265 1270 1275 1280 1285 1290 1295 1300 1305 1310 1315 1320

*
 *
 TAAAGAATTTCATCCCGTA TCACAGTGT TTTATTGCTC GCCCAGACAC CATGTGCAAT
 ATTCTTAAA AGTAGGGCAT AGTGTACAAA AAATAACGAG CGGGTCTGTG GTACACGTTA

1325 1330 1335 1340 1345 1350 1355 1360 1365 1370 1375 1380

*
 *
 AAGATTGGTG TTCGTTTCCA TCATGTCTGT ATACTCCTGT CACCTAGAAC GTGCATCCTT
 TTCTAACACAC AAGCAAAGGT AGTACAGACA TATGAGGACA GTGGATCTTG CACGTAGGAA

1385 1390 1395 1400 1405 1410 1415 1420 1425 1430 1435 1440

*
 *
 GTAATACCTG ATTGATCACA CAGTGTAGT GCTGGTCAGA GAGACCTCAT CCTGCTCTT
 CATTATGGAC TAACTAGTGT GTCAACATCA CGACCAGTCT CTCTGGAGTA GGACGAGAAA

1445 1450 1455 1460 1465 1470 1475 1480 1485 1490 1495 1500

*
 *
 TGTGATGAAC ATATTGATGA AATGTGGAAG TCAGTACGAT CAAGTTGTTG ACTGTGATTA
 ACACTACTTG TATAAGTACT TTACACCTTC AGTCATGCTA GTTCAACAAAC TGACACTAAT

1505 1510 1515 1520 1525 1530 1535 1540 1545 1550 1555 1560

*
 *
 GATCACATCT TAAATTCAATTCTAGACTCA AAACCTGGAG ATGCAGCTAC TGGAATGGTG
 CTAGTGTAGA ATTTAAGTAA AGATCTGAGT TTTGGACCTC TACGTCGATG ACCTTACAC

1565 1570 1575 1580 1585 1590 1595 1600 1605 1610 1615 1620

*
 *
 TTTTGTCAAGA CTTCCAAATC CTGGAAGGAC ACAGTGTGATGA ATGTACTATA TCTGAACATA

FIG. 8 - CONT'D

AAAACAGTCT GAAGGTTTAG GACCTTCCTG TGTCACTACT TACATGATAT AGACTTGTAT
 1625 1630 1635 1640 1645 1650 1655 1660 1665 1670 1675 1680
 * * * * * * * * * * * *
 GAAAACCGGG CTTGAGTGAG AAGAGCTTGC ACAGCCAACG AGACACATTG CCTTCTGGAG
 CTTTGAGCCC GAACTCACTC TTCTCGAACG TGTCGGTTGC TCTGTGTAAC GGAAGACCTC
 1685 1690 1695 1700 1705 1710 1715 1720 1725 1730 1735 1740
 * * * * * * * * * * * *
 CTGGGAGACA AAGGAGGAAT TTACTTTCTT CACCAAGTGC AATAGATTAC TGATGTGATA
 GACCCTCTGT TTCCCTCTTA AATGAAAGAA GTGGTTCAAG TTATCTAATG ACTACACTAT
 1745 1750 1755 1760 1765 1770 1775 1780 1785 1790 1795 1800
 * * * * * * * * * * * *
 TTCTGTTGCT TTACAGTTAC AGTTGATGTT TGGGGATCGA TGTGCTCAGC CAAATTCCT
 AAGACAACGA AATGTCAATG TCAACTACAA ACCCCTAGCT ACACGAGTCG GTTTAAAGGA
 1805 1810 1815 1820 1825 1830 1835 1840 1845 1850 1855 1860
 * * * * * * * * * * * *
 GTTTGAAATA TCATGTTAAA TTAGAATGAA TTTATCTTTA CCAAAACCA TGTTGCGTTC
 CAAACTTTAT AGTACAATT AATCTTACTT AAATAGAAAT GGTTTTGGT ACAACGCAAG
 1865 1870 1875 1880 1885 1890 1895 1900 1905 1910 1915 1920
 * * * * * * * * * * * *
 AAAGAGGTGA ACATTTAAAT ATAGAGACAG GACAGAATGT GTTCTTTCT CCTCTACAG
 TTTCTCCACT TGTAATTAA TATCTCTGTC CTGTCCTACA CAAGAAAAGA GGAGATGGTC
 1925 1930 1935 1940 1945 1950 1955 1960 1965 1970 1975 1980
 * * * * * * * * * * * *
 TCCTATTTT CAATGGGAAG ACTCAGGAGT CTGCCACTTG TCAAAGAAGG TGCTGATCCT
 AGGATAAAAA GTTACCCCTTC TGAGTCCTCA GACGGTGAAC AGTTTCTTCC ACGACTAGGA
 1985 1990 1995 2000 2005 2010 2015 2020 2025 2030 2035 2040
 * * * * * * * * * * * *
 AAGAATTTTT CATTCTCAGA ATTGGTGTG CTGCCACTT GATGTTCCAC CTGCCACAAA
 TTCTTAAAAA GTAAGAGTCT TAAGCCACAC GACGGTTGAA CTACAAGGTG GACGGTGT
 2045 2050 2055 2060 2065 2070 2075 2080 2085 2090 2095 2100
 * * * * * * * * * * * *
 CCACCAGGAC TGAAAGAAGA AAACAGTACA GAAGGCAAAG TTTACAGATG TTTTTAATT
 GGTGGTCCTG ACTTTCTCT TTTGTATGT CTTCCGTTTC AAATGTCTAC AAAATTAAG
 2105 2110 2115 2120 2125 2130 2135 2140 2145 2150 2155 2160
 * * * * * * * * * * * *
 TAGTATTTA TCTGGAACAA CTTGTAGCAG CTATATATT CCCCTTGGTC CCAAGCCTGA
 ATCATAAAAT AGACCTTGTG GAACATCGTC GATATATAAA GGGGAACCAG GGTTCGGACT
 2165 2170 2175 2180 2185 2190 2195 2200 2205 2210 2215 2220
 * * * * * * * * * * * *
 TACTTTAGCC ATCATAACTC ACTAACAGGG AGAAGTAGCT AGTAGCAATG TGCCCTTGATT
 ATGAAATCGG TAGTATTGAG TGATTGTCCC TCTTCATCGA TCATCGTTAC ACGGAACCAA
 2225 2230 2235 2240 2245 2250 2255 2260 2265 2270 2275 2280
 * * * * * * * * * * * *
 GATTAGATAA AGATTTCTAG TAGGCAGCAA AAGACCAAAT CTCAGTTGTT TGCTTCTTGC
 CTAATCTATT TCTAAAGATC ATCCGTCGTT TTCTGGTTA GAGTCACAA ACGAAGAACG
 2285 2290 2295 2300 2305 2310 2315 2320 2325 2330 2335 2340
 * * * * * * * * * * * *
 CATCACTGGT CCAGGTCTTC AGTTTCCGAA TCTCTTTCCC TTCCCCGTG TGCTTATGTC
 GTAGTGACCA GGTCCAGAAG TCAAAGGTT AGAGAAAGGG AAGGGGACAC CAGATAACAG

FIG. 8 - CONT'D

2345	2350	*	2355	2360	*	2365	2370	*	2375	2380	*	2385	2390	*	2395	2400	*
GCTATGTGAC TTGCGCTTAA TCCAATATTT TGCCCTTTTT CTATATCAAA AAACCTTTAC																	
CGATACTG AACGCGAATT AGGTTATAAA ACGGAAAAAA GATATAGTTT TTGGAAATG																	
2405	2410	*	2415	2420	*	2425	2430	*	2435	2440	*	2445	2450	*	2455	2460	*
AGTTAGCAGG GATGTTCCTT ACCGAGGATT TTAAACCCCC AATCTCTCAT AATCGCTAGT																	
TCAATCGTCC CTACAAGGAA TGGCTCCTAA AAATTGGGGG TTAGAGAGTA TTAGCGATCA																	
2465	2470	*	2475	2480	*	2485	2490	*	2495	2500	*	2505	2510	*	2515	2520	*
GTTTAAAAGG CTAAGAACAG TGGGGCCCAA CCGATGTGGT AGGTGATAAA GAGGCATCTT																	
CAAATTTCC GATTCTTATC ACCCCGGGTT GGCTACACCA TCCACTATTT CTCCGTAGAA																	
2525	2530	*	2535	2540	*	2545	2550	*	2555	2560	*	2565	2570	*	2575	2580	*
TTCTAGAGAC ACATTGGACC AGATGAGGAT CCGAAACGGC AGCCCTTACG TTCACTCACCT																	
AAGATCTCTG TGTAAACCTGG TCTACTCCTA GGCTTTGCCG TCGGAAATGC AAGTAGTGGA																	
2585	2590	*	2595	2600	*	2605	2610	*	2615	2620	*	2625	2630	*	2635	2640	*
GCTAGAACCT CTCGTAGTCC ATCACCATTT CTGGCATTT GAATTCTACT GGAAAAAAAT																	
CGATCTTGGA GAGCATCAGG TAGTGGTAAA GAACCGTAAC CTTAAGATGA CCTTTTTTA																	
2645	2650	*	2655	2660	*	2665	2670	*	2675	2680	*	2685	2690	*	2695	2700	*
ACAAAAAGCA AAACAAAACC CTCAGCACTG TTACAAGAGG CCATTTAAGT ATCTTGTGCT																	
TGTTCCTCGT TTTGTTTGG GAGTCGTGAC AATGTTCTCC GGTAAATTCA TAGAACACGA																	
2705	2710	*	2715	2720	*	2725	2730	*	2735	2740	*	2745	2750	*	2755	2760	*
TCTTCACTTA CCCATTAGCC AGGTCTCAT TAGGTTTTGC TTGGGCCTCC CTGGCACTGA																	
AGAAGTGAAT GGGTAATCGG TCCAAGAGTA ATCCAAAACG AACCCGGAGG GACCGTGACT																	
2765	2770	*	2775	2780	*	2785	2790	*	2795	2800	*	2805	2810	*	2815	2820	*
ACCTTACGGCT TTGTATGACA GTGAAGCAGC ACTGTGAGTG GTTCAAGCAC ACTGGAATAT																	
TGGAAATCCGA AACATACTGT CACTTCGTCG TGACACTCAC CAAGTTCGTG TGACCTTATA																	
2825	2830	*	2835	2840	*	2845	2850	*	2855	2860	*	2865	2870	*	2875	2880	*
AAAACAGTCA TGGCCTGAGA TGCAGGTGAT GCCATTACAG AACCAAATCG TGGCACGTAT																	
TTTGTCACT ACCGGACTCT ACGTCCACTA CGGTAATGTC TTGGTTTACG ACCGTGCATA																	
2885	2890	*	2895	2900	*	2905	2910	*	2915	2920	*	2925	2930	*	2935	2940	*
TGCTGTGTCT CCTCTCAGAG TGACAGTCAT AAATACTGTC AAACAATAAA GGGAGAATGG																	
ACGACACAGA GGAGAGTCG ACTGTCACTA TTATGACAG TTGTTATTT CCCTCTTAC																	
2945	2950	*	2955	2960	*	2965	2970	*	2975	2980	*	2985	2990	*	2995	3000	*
TGCTGTAAAGTCACTCC CTGTAATTG CAGAATTCAA AAGTGATTAT CTCTTTGATC																	
ACGACAAATT TCAGTGTAGG GACATTTAAC GTCTTAAGTT TTCACTAATA GAGAAACTAG																	
3005	3010	*	3015	3020	*	3025	3030	*	3035	3040	*	3045	3050	*	3055	3060	*
TACCTGCTC ATTTCCTAT CTTCTCCCCC ACGGTATCCT AAACCTTACA CTCCCCACTG																	
ATGAACGGAG TAAAGGGATA GAAGAGGGGG TGCCATAGGA TTGAAATCT GAAGGGTGAC																	
3065	3070	*	3075	3080	*	3085	3090	*	3095	3100	*	3105	3110	*	3115	3120	*

FIG. 8 - CONT'D

TTCTGAAAGG AGACATTGCT CTATGTCTGC CTTCGACCAC AGCAAGCCAT CATCCTCCAT
AAGACTTCCC TCTGTAACGA GATACAGACG GAAGCTGGTG TCGTTCGGTA GTAGGAGGTA

3125 3130 3135 3140 3145 3150 3155 3160 3165 3170 3175 3180
* * * * * * * * * * * *
TGCTCCCGGG GACTCAAGAG GAATCTGTTT CTCTGCTGTC AACTTCCCCT CTGGCTCAGC
ACGAGGGGCC CTGAGTTCTC CTTAGACAAA GAGACGACAG TTGAAGGGTA GACCGAGTCG

3185 3190 3195 3200 3205 3210 3215 3220 3225 3230 3235 3240
* * * * * * * * * * * *
ATAGGGTCAC TTTGCCATTA TGCAAATGGA GATAAAAGCA ATTCTGGCTG TCCAGGAGCT
TATCCCAGTG AAACGGTAAT ACGTTTACCT CTATTTCTG TAAGACCGAC AGGTCCCTCGA

3245 3250 3255 3260 3265 3270 3275 3280 3285 3290 3295 3300
* * * * * * * * * * * *
AATCTGACCG TTCTATTGTG TGGATGACCA CATAAGAAGG CAATTCTAGT GTATTAATCA
TTAGACTGGC AAGATAAACAC ACCTACTGGT GTATTCTCC GTTAAATCA CATAATTAGT

3305 3310 3315 3320 3325 3330 3335 3340 3345 3350 3355 3360
* * * * * * * * * * * *
TAGATTATTA TAAACTATAA ACTTAAGGGC AAGGAGTTTA TTACAATGTA TCTTTATTAA
ATCTAATAAT ATTTGATATT TGAATTCCCG TTCCTCAAAT AATGTTACAT AGAAATAATT

3365 3370 3375 3380 3385 3390 3395 3400 3405 3410 3415 3420
* * * * * * * * * * * *
AACAAAAGGG TGTATAGTGT TCACAAACTG TGAAAATAGT GTAAGAACTG TACATTGTGA
TTGTTTCCC ACATATCACA AGTGTGAC ACTTTTATCA CATTCTGAC ATGTAACACT

3425 3430 3435 3440 3445 3450 3455 3460 3465 3470 3475 3480
* * * * * * * * * * * *
GCTCTGGTTA TTTTTCTCTT GTACCATAGA AAAATGTATA AAAATTATCA AAAAGCTAAT
CGAGACCAAT AAAAAGAGAA CATGGTATCT TTTTACATAT TTTTAATAGT TTTTCGATTA

3485 3490 3495 3500 3505 3510 3515 3520 3525 3530 3535 3540
* * * * * * * * * * * *
GTGCAGGGAT ATTGCCTTAT TTGTCIGTAA AAAATGGAGC TCAGTAACAT AACTGCTTCT
CACGTCCCTA TAACGGAATA AACAGACATT TTTTACCTCG AGTCATTGTA TTGACGAAGA

3545 3550 3555 3560 3565 3570 3575
* * * * * * * * * * * *
TGGAGCTTG GAATATTTTA TCCTGTATTC TTGTTT (SEQ ID NO:9)
ACCTCGAAC CTTATAAAAT AGGACATAAG AACAAA